

WO 2005/037989

PCT/US2003/024918

45/53

FIG.41A

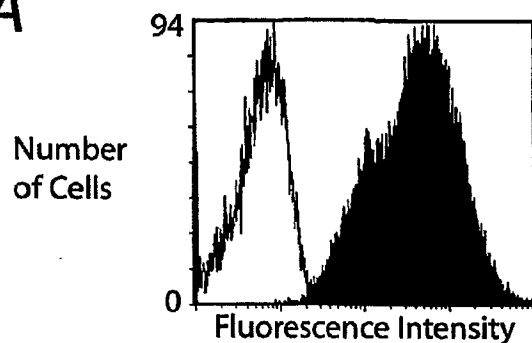


FIG.41B

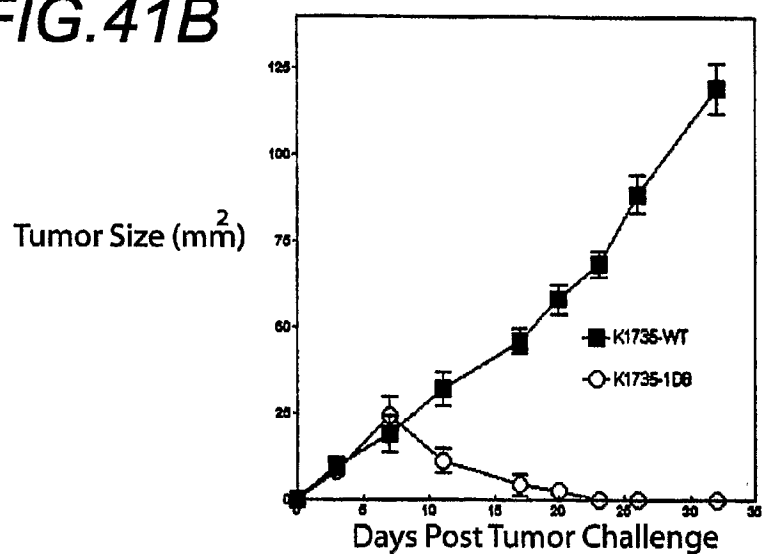
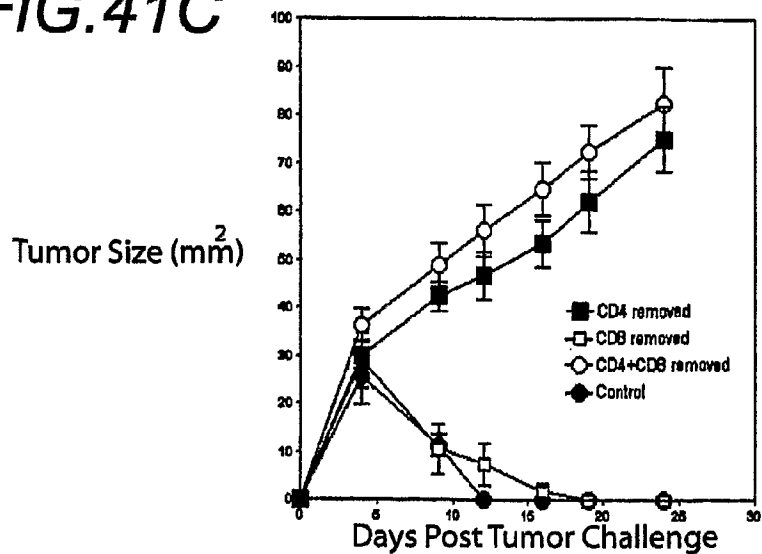


FIG.41C

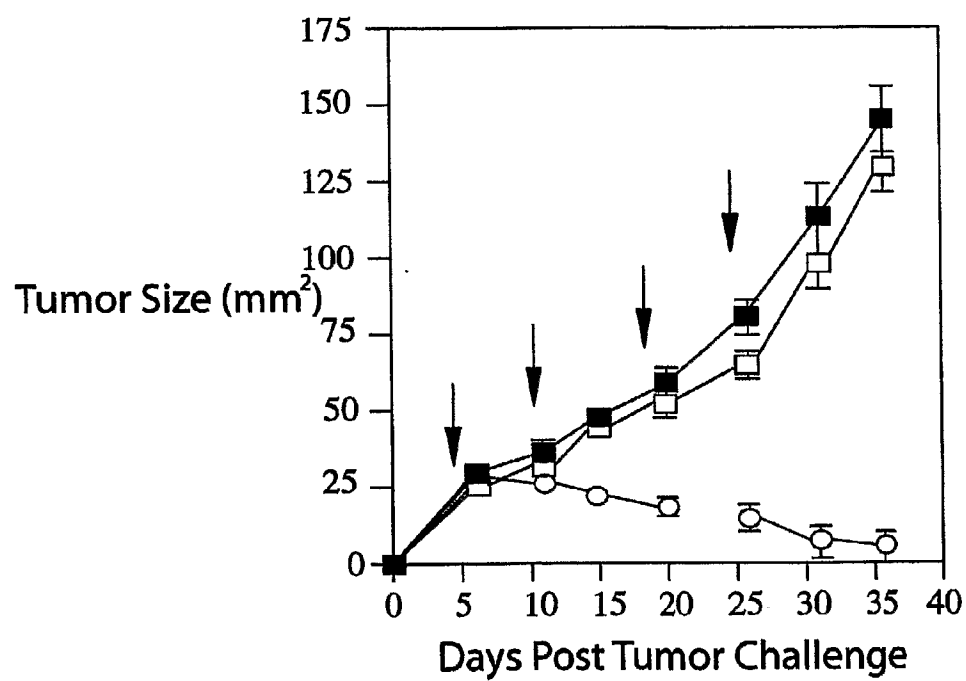


WO 2005/037989

PCT/US2003/024918

46/53

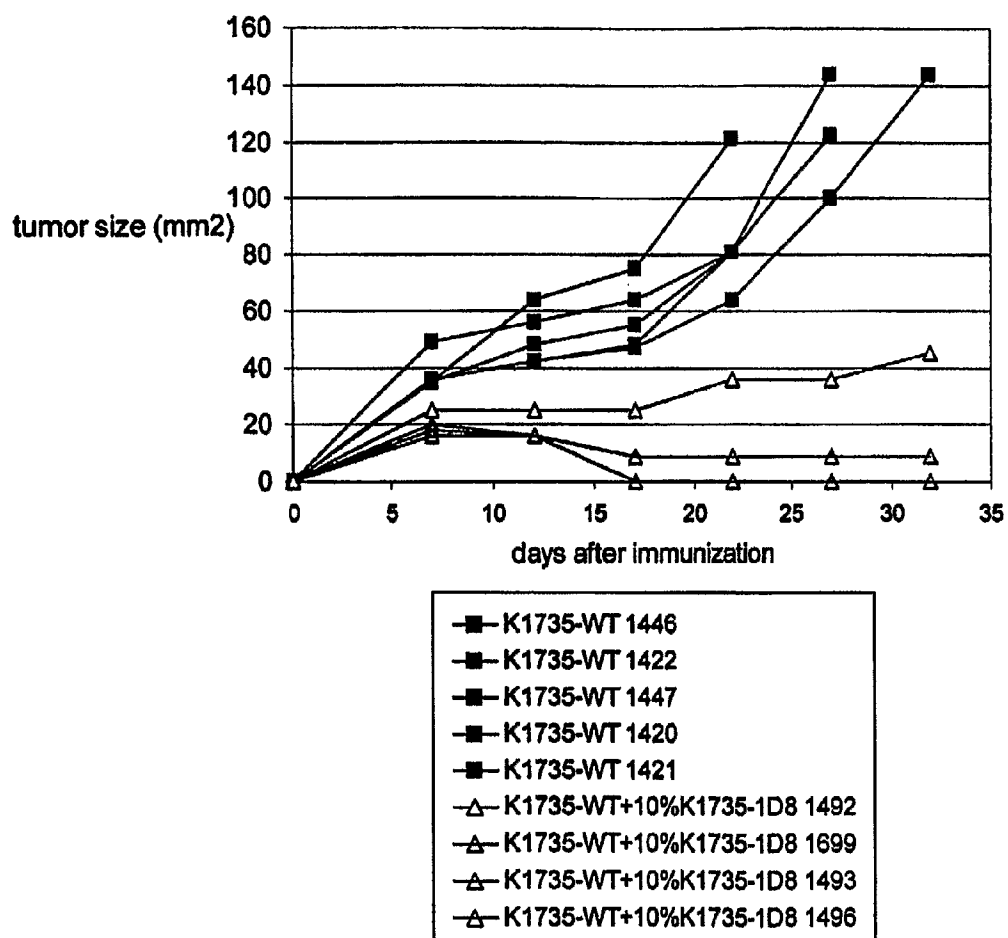
FIG. 42



47/53

FIG.43

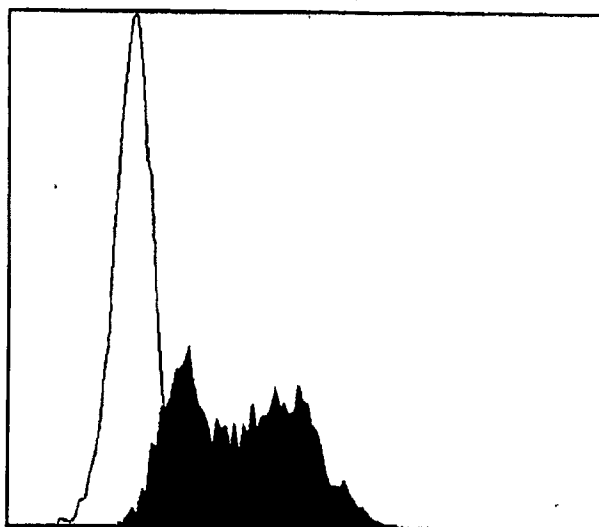
Mixtures of K1735-WT and K1735-1D8 transfected tumor lines
inhibit tumor outgrowth in C3H mice



48/53

FIG. 44

Expression of Anti-CD137 scFvlg on the Surface of
Panned Ag104 Transfected Tumor Cells

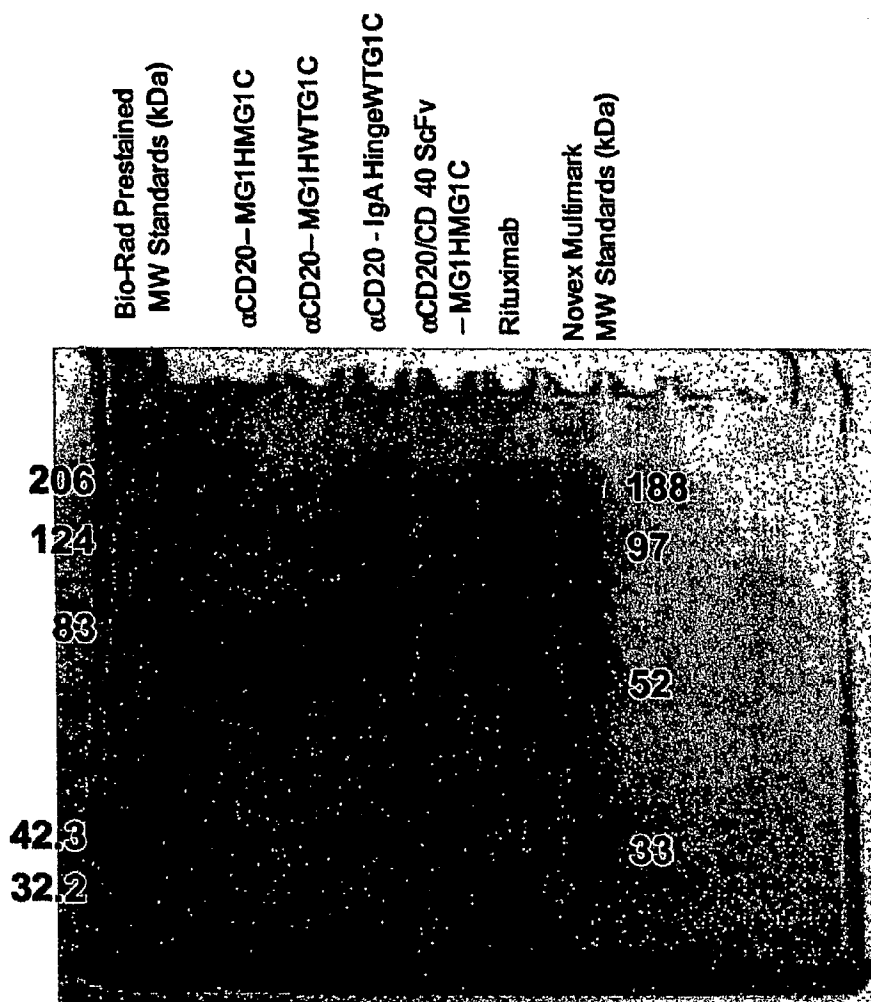


WO 2005/037989

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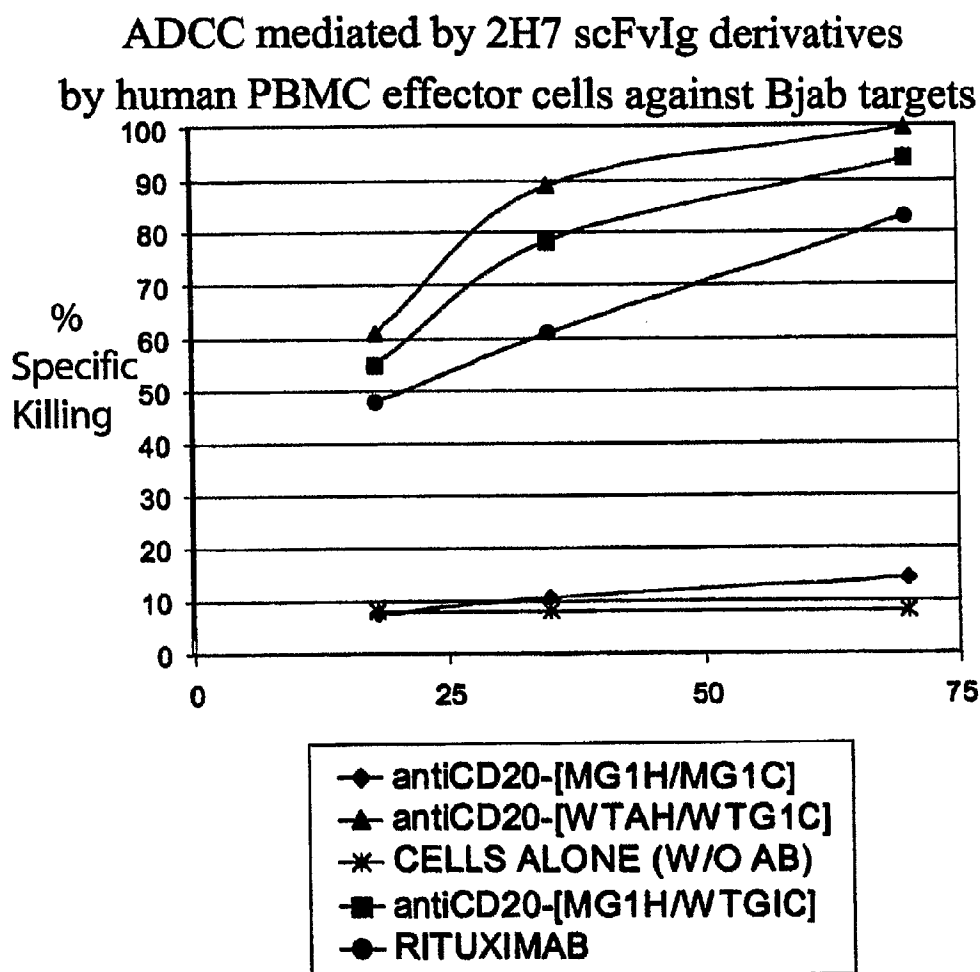
49/53

FIG.45



50/53

FIG.46



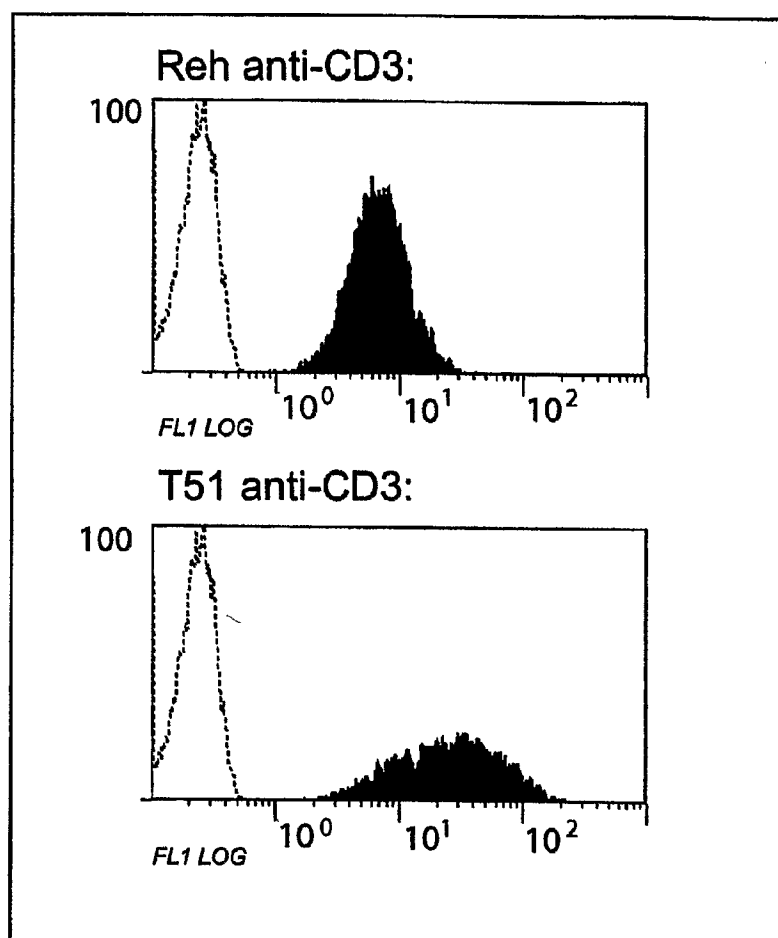
WO 2005/037989

PCT/US2003/024918

51/53

FIG.47

Cell surface expression of anti-human CD3 scFvIg fusion protein on Reh and T51 Cells.



52/53

FIG.48A

Targeting of Cytotoxicity to Transfected Cell Lines
by Surface expression of CD3 scFvIg

Cytotoxic activity of resting PBMC towards transfected Reh cells

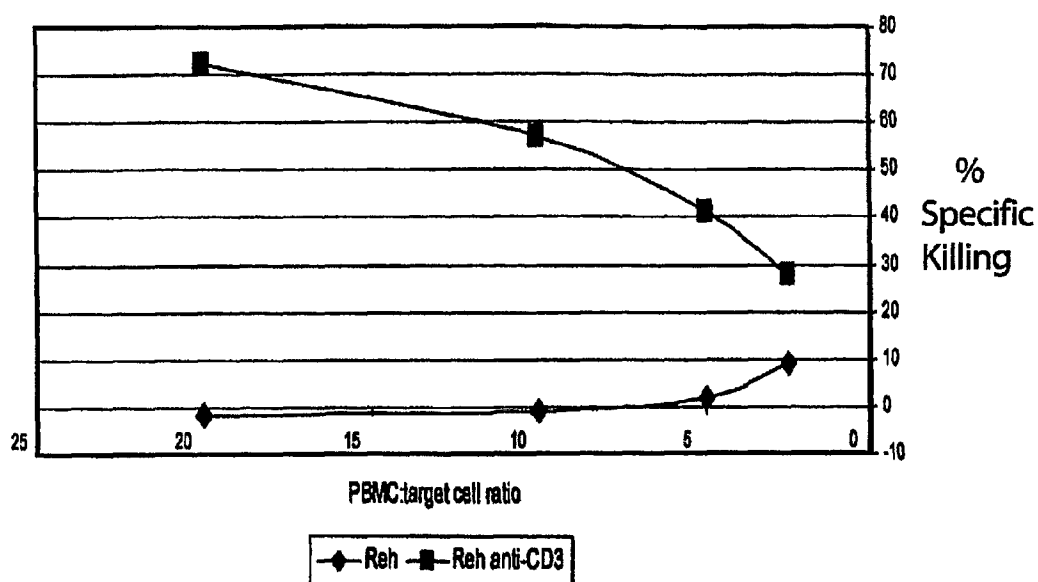
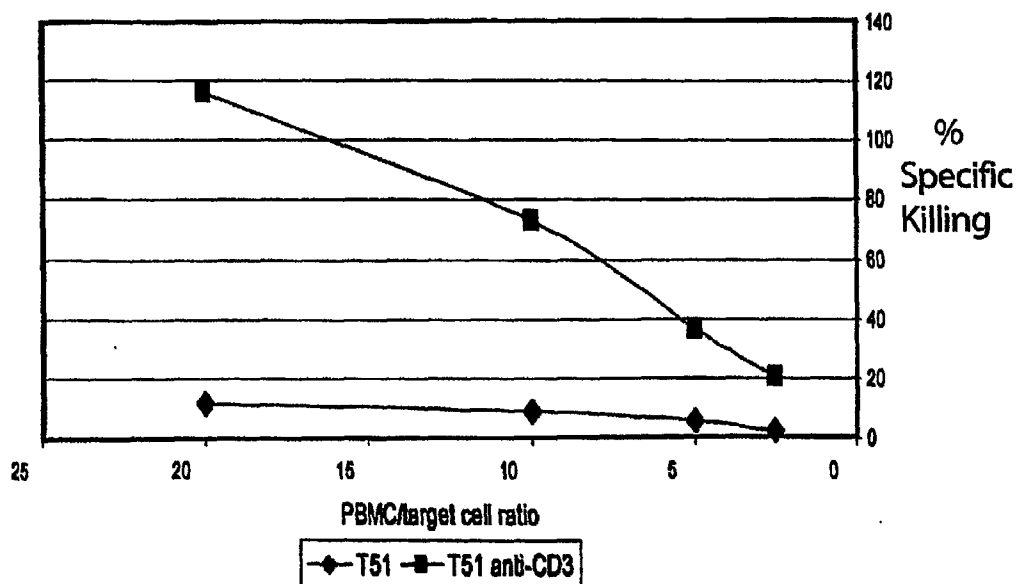


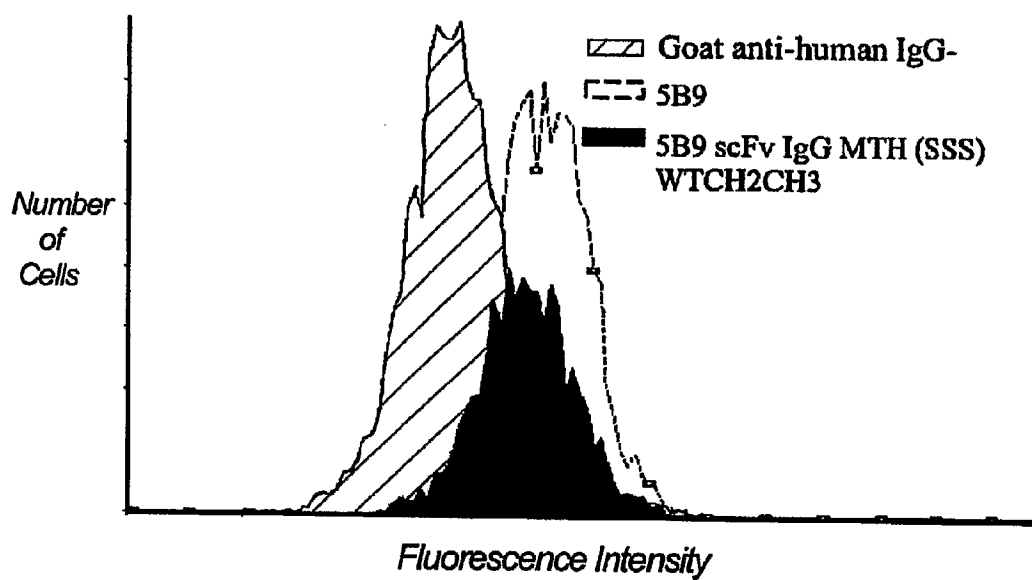
FIG.48B

Cytotoxic activity of resting PBMC towards transfected T51 lymphoblastoid cells



53/53

FIG.49



WO 2005/037989

PCT/US2003/024918

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<170> PatentIn version 3.0

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<220>

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120

ccaggggaga aggtcacaat gacttgcagg gccagctcaa gtgtaagtta catgcactgg
180

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240

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agcagagtgg aggtgaaga tgctgccact tattactgcc agcagtggag ttttaaccca
360

cccacgttcg gtgctgggac caagctggag ctgaaagggt gcggtggctc gggcgggtgt
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WO 2005/037989

PCT/US2003/024918

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WO 2005/037989

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FUNCTION

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WO 2005/037989

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WO 2005/037989

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WO 2005/037989

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WO 2005/037989

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<223> SYNTHETIC MOUSE SCFV FUSION GENE

<220>
<221> misc_feature
<222> (13)..(72)
<223> LIGHT CHAIN LEADER PEPTIDE

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

<220>
<221> V_region
<222> (73)..(405)
<223> LIGHT CHAIN VARIABLE DOMAIN FOR MOUSE ANTI-HUMAN CD19: HD37

<220>
<221> misc_feature
<222> (406)..(450)
<223> SYNTHETIC (GLY4SER)3 LINKER PEPTIDE

<220>
<221> V_region
<222> (454)..(825)
<223> HEAVY CHAIN VARIABLE DOMAIN FOR MOUSE ANTI-HUMAN CD19: HD37

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120
cagagggcca ccatctctg caaggccagc caaagtgttg attatgatgg tgatagttat
180
ttgaactggt accaacagat tccaggacag ccacccaaac tcctcatcta tgatgcatcc
240
aatctagttt ctgggatccc acccaggttt agtggcagtg ggtctgggac agacttcacc
300
ctcaacatcc atcctgtgga gaagggtgat gctgcaacct atcactgtca gcaaagtact
360
gaggatccgt ggacgttcgg tggaggcacc aagctggaaa tcaaagggtg cggtggctcg
420
ggcgggtgtg ggtcgggtgg cggcggatcg tcacaggttc agctgcagca gtctggggct
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gagctgtga ggcctgggtc ctacgtgaag atttcctgca aggccttctg ctatgcattc
540
agtagctact ggatgaactg ggtgaagcag aggcctggac agggcttga gtggattgga
600
cagatttggc ctggagatgg tgatactaac tacaatggaa agttcaaggg taaagccact
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ctgactgcag acgaatcctc cagcacagcc tacatgcaac tcagcagcct agcatctgag
720
gactctgcgg tctatttctg tgcaagacgg gagactacga cggtaggccg ttattactat
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825

<210> 9
<211> 795
<212> DNA
<213> Artificial Sequence

<220>
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<220>
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<222> (13)..(72)
<223> LIGHT CHAIN LEADER PEPTIDE SEQUENCE

<220>
<221> V_region
<222> (73)..(393)
<223> LIGHT CHAIN VARIABLE DOMAIN FOR MOUSE ANTI-HUMAN CD37: G28-1

<220>
<221> misc_feature
<222> (394)..(441)
<223> SYNTHETIC LINKER PEPTIDE ENCODED (GLY4SER)3

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

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<222> (442)..(795)
<223> HEAVY CHAIN VARIABLE DOMAIN FOR MOUSE ANTI-HUMAN CD37: G28-1

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120
gagactgtca ccatcacatg tcgaacaagt gaaaatgttt acagttatatt ggcttgggtat
180
cagcagaaac agggaaaatc tcctcagctc ctgggtctctt ttgcaaaaac cttagcagaa
240
ggtgtgcat caagggtcag tggcagtga tcaggcacac agttttctct gaagatcagc
300
agcctgcagc ctgaagattc tggaagtatt ttctgtcaac atcattccga taatccgtgg
360
acgttcggtg gaggcaccga actggagatc aaagggtggcg gtggctcggg cgggtgggtgg
420
tcgggtggcg gcggatcgtc agcgggtccag ctgcagcagt ctggacctga gctggaaaag
480
cctggcgctt cagtgaagat ttcctgcaag gcttctgggt actcattcac tggctacaat
540
atgaactggg tgaagcagaa taatggaaa agccttgagt ggattggaaa tattgatcct
600
tattatggtg gtactaccta caaccggaag ttcaaggga aggccacatt gactgtagac
660
aaatcctcca gcacagccta catgcagctc aagagtctga catctgagga ctctgcagtc
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780
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795

<210> 10
<211> 824
<212> DNA
<213> Artificial Sequence

<220>
<223> SYNTHETIC MOUSE FUSION GENE

<220>
<221> sig_peptide
<222> (1)..(61)
<223> native light chain leader peptide

<220>
<221> V_region
<222> (62)..(397)
<223> LIGHT CHAIN VARIABLE DOMAIN FOR MOUSE ANTI-HUMAN CD22: G28-7

<220>
<221> misc_feature
<222> (398)..(445)
<223> (gly4ser)3 linker peptide

<220>
<221> V_region
<222> (445)..(818)
<223> HEAVY CHAIN VARIABLE DOMAIN FOR MOUSE ANTI-HUMAN CD22: G28-7

<220>
<221> misc_feature
<222> (819)..(824)
<223> BclI restriction site

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WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

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aacattatga tgacacagtc gccatcatct ctggctgtgt cagcaggaga aaaggtcact
120
atgaactgta agtccagtc aagtgttttc tacagttcaa atcagaggaa ttatttggcc
180
tggtatcagc agaaaccagg gcagtctccc aaattgctga tctactgggc atctactagg
240
gaatctgggtg tccctgatcg cttcacaggc agtggatccg ggacagactt tactcttacc
300
atcagcagtg tacatactga agacctggca gtttattact gtcataaatt cctctcttcg
360
tggaagtctg gtggaggcac caagctggaa atcaaaggcg gtggtggttc ggggtgggtgt
420
ggttcgggtg gcggcggatc ttctcaggtc caactgcagc agcctggggc tgaactgggtg
480
aagcctggga cttcagtga gctgtcctgc aaggcctctg gctacacctt caccaactac
540
tggaagtctg ggggtgaagca gacgcctgga gaaggccttg agtggattgg agaaattatt
600
cctagcaacg gtcgtactaa atacaatgag aagttcaaga gcaaggccac actgactgca
660
gacaaatcct cccgcacagc ctacatgcaa ctacagagcc tggcatctga ggactctgcg
720
gtctattatt gtgcaagaga gatgtccatt attactacgg tactgactcc cggtttgctt
780
actggggcca agggactctg gtcactgtct ctgcagcctg atca
824
```

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<210> 11
<211> 266
<212> PRT
<213> Mus musculus
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<220>
<221> INIT_MET
<222> (1)..(1)
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<220>
<221> SIGNAL
<222> (1)..(22)
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<220>
<221> DOMAIN
<222> (23)..(128)
<223> LIGHT CHAIN VARIABLE DOMAIN FOR MOUSE ANTI-HUMAN CD20
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<220>
<221> SITE
<222> (129)..(144)
<223> ASP-(GLY3SER)-(GLY4SER)2-SER LINKER PEPTIDE
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<220>
<221> DOMAIN
<222> (145)..(266)
<223> HEAVY CHAIN VARIABLE DOMAIN FOR MOUSE ANTI-HUMAN CD20
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<400> 11
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1           5           10           15
Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
20           25           30
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
35           40           45
ser ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
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WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 50 | Pro | Lys | Pro | Trp | Ile | Tyr | Ala | Pro | Ser | Asn | Leu | Ala | Ser | Gly | Val | Pro |
| 65 | Ala | Arg | Phe | Ser | Gly | Ser | Gly | Ser | Gly | Thr | Ser | Tyr | Ser | Leu | Thr | Ile |
| | | | | 85 | Ala | Glu | Asp | Ala | Ala | Thr | Tyr | Tyr | Cys | Gln | Gln | Trp |
| | Ser | Phe | Asn | Pro | Thr | Phe | Gly | Ala | Gly | Thr | Lys | Leu | Glu | Leu | Lys | |
| | 115 | Gly | Gly | Ser | Gly | Gly | Gly | Gly | Ser | Gly | Gly | Gly | Gly | Ser | Ser | |
| | 130 | Ala | Tyr | Leu | Gln | Gln | Ser | Gly | Ala | Glu | Leu | Val | Arg | Pro | Gly | Ala |
| 145 | Ser | Val | Lys | Met | Ser | Cys | Lys | Ala | Ser | Gly | Tyr | Thr | Phe | Thr | Ser | Tyr |
| | | | | 165 | Val | Lys | Gln | Thr | Pro | Arg | Gln | Gly | Leu | Glu | Trp | Ile |
| | Gly | Ala | Ile | Tyr | Pro | Gly | Asn | Gly | Asp | Thr | Ser | Tyr | Asn | Gln | Lys | Phe |
| | 195 | Lys | Lys | Ala | Thr | Leu | Thr | Val | Asp | Lys | Ser | Ser | Ser | Thr | Ala | Tyr |
| | 210 | Met | Gln | Leu | Ser | Ser | Leu | Thr | Ser | Glu | Asp | Ser | Ala | Val | Tyr | Phe |
| 225 | Ala | Arg | Val | Val | Tyr | Tyr | Ser | Asn | Ser | Tyr | Trp | Tyr | Phe | Asp | Val | Trp |
| | | | | 245 | Thr | Val | Thr | Val | Ser | Asp | | | | | | |
| | Gly | Thr | Gly | Thr | Thr | Val | Thr | Val | Ser | Asp | | | | | | |
| | | | | 260 | | | | | | | | | | | | |

<210> 12
 <211> 271
 <212> PRT
 <213> Mus musculus
 <220>
 <221> SITE
 <222> (1)..(271)
 <223> MOUSE ANTI-HUMAN CD19 SCFV

<400> 12

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Thr | Asp | Thr | Leu | Leu | Leu | Trp | Val | Leu | Leu | Leu | Trp | Val | Pro |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Gly | Ser | Thr | Gly | Asp | Ile | Val | Leu | Thr | Gln | Ser | Pro | Ala | Ser | Leu | Ala |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Val | Ser | Leu | Gly | Gln | Arg | Ala | Thr | Ile | Ser | Cys | Lys | Ala | Ser | Gln | Ser |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Val | Asp | Tyr | Asp | Gly | Asp | Ser | Tyr | Leu | Asn | Trp | Tyr | Gln | Gln | Ile | Pro |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Gly | Gln | Pro | Pro | Lys | Leu | Leu | Ile | Tyr | Asp | Ala | Ser | Asn | Leu | Val | Ser |
| 65 | | | | 70 | | | | | 75 | | | | | 80 | |
| Gly | Ile | Pro | Pro | Arg | Phe | Ser | Gly | Ser | Gly | Ser | Gly | Thr | Asp | Phe | Thr |
| | | | | 85 | | | | 90 | | | | | | 95 | |
| Leu | Asn | Ile | His | Pro | Val | Glu | Lys | Val | Asp | Ala | Ala | Thr | Tyr | His | Cys |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Gln | Gln | Ser | Thr | Glu | Asp | Pro | Trp | Thr | Phe | Gly | Gly | Gly | Thr | Lys | Leu |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Glu | Ile | Lys | Gly | Gly | Gly | Gly | Ser | Gly | Gly | Gly | Gly | Ser | Gly | Gly | Gly |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Gly | Ser | Ser | Gln | Val | Gln | Leu | Gln | Gln | Ser | Gly | Ala | Glu | Leu | Val | Arg |
| 145 | | | | 150 | | | | | 155 | | | | | 160 | |
| Pro | Gly | Ser | Ser | Val | Lys | Ile | Ser | Cys | Lys | Ala | Ser | Gly | Tyr | Ala | Phe |
| | | | | 165 | | | | 170 | | | | | | 175 | |
| Ser | Ser | Tyr | Trp | Met | Asn | Trp | Val | Lys | Gln | Arg | Pro | Gly | Gln | Gly | Leu |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Glu | Trp | Ile | Gly | Gln | Ile | Trp | Pro | Gly | Asp | Gly | Asp | Thr | Asn | Tyr | Asn |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Gly | Lys | Phe | Lys | Gly | Lys | Ala | Thr | Leu | Thr | Ala | Asp | Glu | Ser | Ser | Ser |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Thr | Ala | Tyr | Met | Gln | Leu | Ser | Ser | Leu | Ala | Ser | Glu | Asp | Ser | Ala | Val |

WO 2005/037989

PCT/US2003/024918

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225 230 235 240
Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr
245 250 255
Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
260 265 270

<210> 13
<211> 259
<212> PRT
<213> Mus musculus

<220>
<221> SITE
<222> (1)..(259)
<223> MOUSE ANTI-HUMAN CD37 SCFV

<400> 13

Met Val Ser Thr Ala Gln Phe Leu Gly Leu Leu Leu Leu Trp Leu Thr
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20 25 30
Ala Ser Val Gly Glu Thr Val Thr Ile Thr Cys Arg Thr Ser Glu Asn
35 40 45
Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro
50 55 60
Gln Leu Leu Val Ser Phe Ala Lys Thr Leu Ala Glu Gly Val Pro Ser
65 70 75 80
Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Phe Ser Leu Lys Ile Ser
85 90 95
Ser Leu Gln Pro Glu Asp Ser Gly Ser Tyr Phe Cys Gln His His Ser
100 105 110
Asp Asn Pro Trp Thr Phe Gly Gly Gly Thr Glu Leu Glu Ile Lys Gly
115 120 125
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Ala
130 135 140
Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Glu Lys Pro Gly Ala Ser
145 150 155 160
Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr Asn
165 170 175
Met Asn Trp Val Lys Gln Asn Asn Gly Lys Ser Leu Glu Trp Ile Gly
180 185 190
Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe Lys
195 200 205
Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr Met
210 215 220
Gln Leu Lys Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala
225 230 235 240
Arg Ser Val Gly Pro Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr
245 250 255
Val Ser Ser

<210> 14
<211> 272
<212> PRT
<213> Mus musculus

<220>
<221> SITE
<222> (1)..(272)
<223> MOUSE ANTI-HUMAN CD22 SCFV

<400> 14

Met Glu Ser His Ser Gln Val Phe Leu Ser Leu Leu Leu Trp Val Ser
1 5 10 15
Gly Thr Cys Gly Asn Ile Met Met Thr Gln Ser Pro Ser Ser Leu Ala

WO 2005/037989

PCT/US2003/024918

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| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ser | Ala | Gly | Glu | Lys | Val | Thr | Met | Asn | Cys | Lys | Ser | Ser | Gln | Ser |
| | | 20 | | | | | 25 | | | | | 30 | | | |
| Val | Phe | 35 | Tyr | Ser | Ser | Asn | Gln | 40 | Asn | Tyr | Leu | Ala | 45 | Tyr | Gln |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Lys | Pro | Gly | Gln | Ser | Pro | Lys | Leu | Leu | Ile | Tyr | 75 | Trp | Ala | Ser | Thr |
| 65 | | | | | 70 | | | | | | | | | | 80 |
| Glu | Ser | Gly | Val | Pro | Asp | Arg | Phe | Thr | Gly | Ser | Gly | Ser | Gly | Thr | Asp |
| | | | 85 | | | | | | 90 | | | | | 95 | |
| Phe | Thr | Leu | Thr | Ile | Ser | Ser | Val | His | 105 | Thr | Glu | Asp | Leu | Ala | Val |
| | | | 100 | | | | | | | | | | | 110 | |
| Tyr | Cys | His | Gln | Phe | Leu | Ser | Ser | Trp | Thr | Phe | Gly | Gly | Gly | Thr | Lys |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Leu | Glu | Ile | Lys | Gly | Gly | Gly | Gly | Ser | Gly | Gly | Gly | Gly | Ser | Gly | Gly |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Gly | Gly | Ser | Ser | Gln | Val | Gln | Leu | Gln | Gln | Pro | 155 | Gly | Ala | Glu | Val |
| 145 | | | | | 150 | | | | | | | | | | 160 |
| Lys | Pro | Gly | Thr | Ser | Val | Lys | Leu | Ser | Cys | Lys | Ala | Ser | Gly | Tyr | Thr |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| Phe | Thr | Asn | Tyr | Trp | Met | Val | Trp | Val | Lys | Gln | Thr | Pro | Gly | Glu | Gly |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Leu | Glu | Trp | Ile | Gly | Glu | Ile | Ile | Pro | Ser | Asn | Gly | Arg | Thr | Lys | Tyr |
| | | 195 | | | | | 200 | | | | | | | | |
| Asn | Glu | Lys | Phe | Lys | Ser | Lys | Ala | Thr | Leu | Thr | Ala | Asp | Lys | Ser | Ser |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Arg | Thr | Ala | Tyr | Met | Gln | Leu | Ser | Ser | Leu | Ala | Ser | Glu | Asp | Ser | Ala |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 |
| Val | Tyr | Tyr | Cys | Ala | Arg | Glu | Met | Ser | Ile | Ile | Thr | Thr | Val | Leu | Thr |
| | | | 245 | | | | | | 250 | | | | | 255 | |
| Pro | Gly | Leu | Leu | Thr | Gly | Ala | Lys | Gly | Leu | Trp | Ser | Leu | Ser | Leu | Gln |
| | | | 260 | | | | | 265 | | | | | 270 | | |

<210> 15
<211> 499
<212> PRT
<213> Artificial Sequence

<220>
<223> MOUSE-HUMAN HYBRID FUSION PROTEIN

<220>
<221> SITE
<222> (1)..(265)
<223> MOUSE ANTI-HUMAN CD20 SCFV: 2H7

<220>
<221> DOMAIN
<222> (266)..(499)
<223> HUMAN IGG1 WILD TYPE HINGE, CH2, CH3 FC

<400> 15

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Phe | Gln | Val | Gln | Ile | Phe | Ser | Phe | Leu | Leu | Ile | Ser | Ala | Ser |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Val | Ile | Ile | Ala | Arg | Gly | Gln | Ile | Val | Leu | Ser | Gln | Ser | Pro | Ala | Ile |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Leu | Ser | Ala | Ser | Pro | Gly | Glu | Lys | Val | Thr | Met | Thr | Cys | Arg | Ala | Ser |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Ser | Ser | Val | Ser | Tyr | Met | His | Trp | Tyr | Gln | Gln | Lys | Pro | Gly | Ser | Ser |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Pro | Lys | Pro | Trp | Ile | Tyr | Ala | Pro | Ser | Asn | Leu | Ala | Ser | Gly | Val | Pro |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Ala | Arg | Phe | Ser | Gly | Ser | Gly | Ser | Gly | Thr | Ser | Tyr | Ser | Leu | Thr | Ile |
| | | | 85 | | | | | | 90 | | | | | 95 | |
| Ser | Arg | Val | Glu | Ala | Glu | Asp | Ala | Ala | Thr | Tyr | Tyr | Cys | Gln | Gln | Trp |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Ser | Phe | Asn | Pro | Pro | Thr | Phe | Gly | Ala | Gly | Thr | Lys | Leu | Glu | Leu | Lys |
| | | 115 | | | | | 120 | | | | | 125 | | | |

WO 2005/037989

PCT/US2003/024918

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 Asp Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser
 130 135 140
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
 145 150 155 160
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 165 170 175
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
 180 185 190
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
 195 200 205
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr
 210 215 220
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 225 230 235 240
 Ala Arg Val Val Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
 245 250 255
 Gly Thr Gly Thr Thr Val Thr Val Ser Asp Gln Glu Pro Lys Ser Cys
 260 265 270
 Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 275 280 285
 Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 290 295 300
 Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Asp Val Ser His
 305 310 315 320
 Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 325 330 335
 His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
 340 345 350
 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 355 360 365
 Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
 370 375 380
 Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 385 390 395 400
 Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
 405 410 415
 Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 420 425 430
 Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 435 440 445
 Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 450 455 460
 Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 465 470 475 480
 His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 485 490 495
 Pro Gly Lys

<210> 16
 <211> 499
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MOUSE-HUMAN HYBRID FUSION PROTEIN

<220>
 <221> SITE
 <222> (1)..(265)
 <223> 2H7 SCFV TARGETED TO HUMAN CD20

<220>
 <221> DOMAIN
 <222> (265)..(499)
 <223> HINGE CYSTEINES MUTATED TO SERINES (AMINO ACIDS 272, 278, 281)
 PROLINE IN CH2 MUTATED TO SERINE (AMINO ACID 290)

<400> 16

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

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Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
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Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
20      25      30
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
35      40      45
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
50      55      60
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
65      70      75      80
Ala Arg Phe Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
85      90      95
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
100     105
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
115     120     125
Asp Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Ser
130     135     140
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
145     150     155     160
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
165     170     175
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
180     185     190
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
195     200     205
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr
210     215     220
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
225     230     235     240
Ala Arg Val Val Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
245     250     255
Gly Thr Gly Thr Thr Val Thr Val Ser Asp Gln Glu Pro Lys Ser Ser
260     265     270
Asp Lys Thr His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly
275     280     285
Gly Ser Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
290     295     300
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Asp Val Ser His
305     310     315     320
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
325     330     335
His Asn Ala Lys Thr Lys Pro Arg Glu Gln Tyr Asn Ser Thr Tyr
340     345     350
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
355     360     365
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
370     375     380
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
385     390     395     400
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
405     410     415
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
420     425     430
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
435     440     445
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
450     455     460
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
465     470     475     480
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
485     490     495
Pro Gly Lys

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<210> 17
<211> 499
<212> PRT

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
<213> Artificial Sequence

<220>

<223> MOUSE-HUMAN HYBRID FUSION PROTEIN

<220>

<221> SITE

<222> (1)..(265)

<223> MOUSE ANTI-HUMAN CD20 SCFV: 2H7

<220>

<221> DOMAIN

<222> (266)..(499)

<223> HINGE CYSTEINES MUTATED TO SERINES (AMINO ACIDS 272, 278, 281)
CH2 AND CH3 DOMAINS ARE WILD TYPE IN SEQUENCE

<400> 17

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Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1      5      10      15
Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
20      25      30
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
35      40      45
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
50      55      60
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
65      70      75      80
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
85      90      95
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
100     105     110
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
115     120     125
Asp Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser
130     135     140
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
145     150     155     160
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
165     170     175
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
180     185     190
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
195     200     205
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr
210     215     220
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
225     230     235     240
Ala Arg Val Val Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
245     250     255
Gly Thr Gly Thr Thr Val Thr Val Ser Asp Gln Glu Pro Lys Ser Ser
260     265     270
Asp Lys Thr His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly
275     280     285
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
290     295     300
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Asp Val Ser His
305     310     315     320
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
325     330     335
His Asn Ala Lys Thr Lys Pro Arg Glu Gln Tyr Asn Ser Thr Tyr
340     345     350
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
355     360     365
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
370     375     380
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
385     390     395     400

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WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
405 410 415
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
420 425 430
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
435 440 445
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
450 455 460
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
465 470 475 480
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
485 490 495
Pro Gly Lys

<210> 18

<211> 505

<212> PRT

<213> Artificial Sequence

<220>

<223> MOUSE-HUMAN FUSION PROTEIN

<220>

<221> SITE

<222> (1)..(265)

<223> MOUSE ANTI-HUMAN CD20 SCFV: 2H7

<220>

<221> DOMAIN

<222> (266)..(288)

<223> WILD TYPE IGA HINGE

<220>

<221> DOMAIN

<222> (289)..(505)

<223> HUMAN IGG1 CH2 AND CH3 DOMAINS, WILD TYPE SEQUENCE

<400> 18

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
20 25 30
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
35 40 45
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
50 55 60
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
65 70 75 80
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
85 90 95
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
100 105 110
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
115 120 125
Asp Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser
130 135 140
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
145 150 155 160
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
165 170 175
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
180 185 190
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
195 200 205
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr
210 215 220
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 225 230 235 240
 Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
 Gly Thr Gly Thr Thr Val Thr Val Ser Asp Gln Pro Val Pro Ser Thr
 Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Cys
 Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
 Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 Lys Ser Leu Ser Leu Ser Pro Gly Lys
 500 505

<210> 19
 <211> 234
 <212> PRT
 <213> Homo sapiens

<220>
 <221> DOMAIN
 <222> (1)..(234)
 <223> MUTANT IGG1 HINGE (AMINO ACIDS 7, 13, 16)
 WILD TYPE CH2 AND CH3 DOMAINS
 ALTERNATIVE CARBOXY TERMINUS OF SCFVIG FUSION PROTEINS

<400> 19

Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Ser
 1 5 10 15
 Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
 20 25 30
 Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
 35 40 45
 Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
 50 55 60
 Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
 65 70 75 80
 Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
 85 90 95
 His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
 100 105 110
 Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
 115 120 125
 Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
 130 135 140
 Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
145 150 155 160
Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
165 170 175
Asn Tyr Lys Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
180 185 190
Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
195 200 205
Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
210 215 220
Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 20
<211> 240
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (1)..(23)
<223> ALTERNATIVE CARBOXY TERMINUS OF SCFVIG FUSION PROTEINS

<220>
<221> DOMAIN
<222> (24)..(240)
<223> HUMAN IGG1 WILD TYPE CH2 AND CH3 FC

<400> 20

Asp Gln Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro
1 5 10 15
Pro Thr Pro Ser Pro Ser Cys Ala Pro Glu Leu Leu Gly Gly Pro Ser
20 25 30
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
35 40 45
Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
50 55 60
Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
65 70 75 80
Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
85 90 95
Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
100 105 110
Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
115 120 125
Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
130 135 140
Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
145 150 155 160
Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
165 170 175
Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
180 185 190
Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
195 200 205
Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
210 215 220
Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
225 230 235 240

<210> 21
<211> 1470
<212> DNA
<213> Artificial Sequence

<220>
<223> MOUSE-HUMAN HYBRID

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

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<220>
<221> misc_feature
<222> (1)..(808)
<223> MOUSE ANTI-HUMAN CD20 SCFV

<220>
<221> misc_feature
<222> (814)..(1455)
<223> HUMAN EXTRACELLULAR DOMAIN LONG FORM, CD154

<400> 21
aagcttgccg ccatggattt tcaagtgcag attttcagct tcctgctaata cagtgtctca
60
gtcataattg ccagaggaca aattgttctc tcccagcttc cagcaatcct gtctgcatct
120
ccaggggaga aggtcacaat gacttgacag gccagctcaa gtgtaagtta catgcactgg
180
taccagcaga agccaggatc ctccccaaa ccctggattt atgccccatc caacctggct
240
tctggagtcg ctgctcgctt cagtggcagt ggggtctggga cctcttactc tctcacaatc
300
agcagagtgg aggtgaaga tgctgccact tattactgcc agcagtggag ttttaaccca
360
cccacgttcg gtgctgggac caagctggag ctgaaagatg gcgggtggctc gggcggtggg
420
ggatctggag gaggtgggag ctctcaggct tatctacagc agtctggggc tgagctgggtg
480
aggcctgggg cctcagtga gatgtcctgc aaggcttctg gctacacatt taccagttac
540
aatatgcact gggtaaagca gacacctaga cagggcctgg aatggattgg agctatttat
600
ccaggaaatg gtgatacttc ctacaatcag aagttcaagg gcaaggccac actgactgta
660
gacaaatcct ccagcacagc ctacatgcag ctacagagcc tgacatctga agactctgcg
720
gtctatttct gtgcaagagt ggtgtactat agtaactctt actgggtactt cgatgtctgg
780
ggcacaggga ccacggtcac cgtctctgat ccaagaagg tggacaagat agaagatgaa
840
aggaatcttc atgaagattt tgtattcatg aaaacgatac agagatgcaa cacaggagaa
900
agatccttat ccttactgaa ctgtgaggag attaaaagcc agtttgaaagg ctttgtgaag
960
gatataatgt taaacaaaga ggagacgaag aaagaaaaca gctttgaaat gcaaaaagg
1020
gatcagaatc ctcaaattgc ggcacatgtc ataagtgagg ccagcagtaa aacaacatct
1080
gtgttacagt gggctgaaa aggatactac accatgagca acaacttggg aaccttgga
1140
aatgggaaac agctgaccgt taaaagacaa ggactctatt atatctatgc ccaagtcacc
1200
ttctgttcca atcggaagc ttcgagtcaa gctccattta tagccagcct ctgcctaaag
1260
tccccggta gattcgagag aatcttactc agagctgcaa ataccacag ttccgcaaaa
1320
ccttgcgggc aacaatccat tcactgggga ggagtatttg aattgcaacc aggtgcttcg
1380
gtgtttgtca atgtgactga tccaagccaa gtgagccatg gcactggctt cacgtccttt
1440
ggcttactca aactcgagtg ataacttaga
1470

<210> 22
<211> 1290
<212> DNA
<213> Artificial Sequence

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WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

<220>

<223> MOUSE-HUMAN HYBRID

<220>

<221> misc_feature

<222> (13)..(808)

<223> MOUSE ANTI-HUMAN CD20 SCFV

<220>

<221> misc_feature

<222> (814)..(1275)

<223> HUMAN EXTRACELLULAR DOMAIN, SHORT FORM, CD154

<400> 22

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aagcttgccg ccatggattt tcaagtgcag attttcagct tcctgctaata cagtgcattca
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gtcataattg ccagaggaca aattgttctc tcccagtcct cagcaatcct gtctgcatct
120
ccaggggaga aggtcacaat gacttgcagg gccagctcaa gtgtaagtta catgactagg
180
taccagcaga agccaggatc ctccccaaa ccctggattt atgccccatc caacctggct
240
tctggagtcg ctgctcgctt cagtggcagt gggctctggga cctcttactc tctcacaatc
300
agcagagtgg aggtgaaga tgctgccact tattactgcc agcagtggag ttttaaccca
360
cccacgttcg gtgctgggac caagctggag ctgaaagatg gcggtggctc gggcggtggt
420
ggatctggag gaggtgggag ctctcaggct tatctacagc agtctggggc tgagctgggt
480
aggcctgggg cctcagtga gatgtcctgc aaggcttctg gctacacatt taccagttac
540
aatatgcact gggtaaagca gacacctaga cagggcctgg aatggattgg agctatttat
600
ccaggaaatg gtgatacttc ctacaatcag aagttcaagg gcaaggccac actgactgta
660
gacaaatcct ccagcacagc ctacatgcag ctacagcagc tgacatctga agactctgag
720
gtctatttct gtgcaagagt ggtgtactat agtaactctt actggtactt cgatgtctgg
780
ggcacaggga ccacggtcac cgtctctgat ccagaaaaca gctttgaaat gcaaaaagg
840
gatcagaatc ctcaaattgc ggcacatgac ataagtggag ccagcagtaa aacaacatct
900
gtgttacagt gggctgaaaa aggatactac accatgagca acaacttggg aacctggaa
960
aatgggaaac agctgaccgt taaaagacaa ggactctatt atatctatgc ccaagtcacc
1020
ttctgttcca atcgggaagc ttcgagtcac gctccattta tagccagcct ctgcctaaag
1080
tcccccggtg gattcgagag aatcttactc agagctgcaa ataccacag ttccgccaaa
1140
ccttgcgggc aacaatccat tcaactggga ggagtatttg aattgcaacc aggtgcttcg
1200
gtgtttgtca atgtgactga tccaagccaa gtgagccatg gcactggctt cacgtccttt
1260
ggcttactca aactcgagtg ataactaga
1290
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<210> 23

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> OLIGONUCLEOTIDE

<400> 23

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
gtcaagcttg ccgcatgga tttcaagtg cagatttttc agc
43

<210> 24
<211> 74
<212> DNA
<213> Artificial Sequence

<220>
<223> OLIGONUCLEOTIDE

<400> 24
gtcgtcgagc tcccacctcc tccagatcca ccaccgccc agccaccgcc acctttcagc
60
tccagcttgg tccc
74

<210> 25
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> OLIGONUCLEOTIDE

<400> 25
gctgctgagc tctcaggctt atctacagca agtctgg
37

<210> 26
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> OLIGONUCLEOTIDE

<400> 26
gttgctgat cagagacggt gaccgtgggc cc
32

<210> 27
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> OLIGONUCLEOTIDE

<400> 27
gttgctggat ccagaaaaca gctttgaaat gcaa
34

<210> 28
<211> 44
<212> DNA
<213> Artificial Sequence

<220>

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
<223> OLIGONUCLEOTIDE

<400> 28
gttgtttcta gattatcact cgagtttgag taagccaaag gacg
44

<210> 29
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> OLIGONUCLEOTIDE

<400> 29
gttggtcggat ccaagaaggt tggacaagat agaag
35

<210> 30
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> OLIGONUCLEOTIDE

<400> 30
gtctatataa gcagagctct ggc
23

<210> 31
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> OLIGONUCLEOTIDE

<400> 31
cgaggctgat cagcgagctc tagca
25

<210> 32
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> OLIGONUCLEOTIDE

<400> 32
ccgcaatttg aggattctga tcacc
25

<210> 33
<211> 482
<212> PRT
<213> Artificial Sequence

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

<220>

<223> MOUSE-HUMAN HYBRID FUSION PROTEIN

<220>

<221> SITE

<222> (1)..(266)

<223> MOUSE ANTI-HUMAN CD20 SCFV

<220>

<221> DOMAIN

<222> (268)..(481)

<223> EXTRACELLULAR DOMAIN, LONG FORM, HUMAN CD154

<400> 33

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Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1      5      10      15
Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
20      25      30
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
35      40      45
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
50      55      60
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
65      70      75      80
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
85      90      95
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
100     105     110
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
115     120     125
Asp Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser
130     135     140
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
145     150     155     160
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
165     170     175
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
180     185     190
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
195     200     205
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr
210     215     220
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
225     230     235     240
Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
245     250     255
Gly Thr Gly Thr Val Thr Val Ser Asp Pro Arg Arg Leu Asp Lys
260     265     270
Ile Glu Asp Glu Arg Asn Leu His Glu Asp Phe Val Phe Met Lys Thr
275     280     285
Ile Gln Arg Cys Asn Thr Gly Glu Arg Ser Leu Ser Leu Leu Asn Cys
290     295     300
Glu Glu Ile Lys Ser Gln Phe Glu Gly Phe Val Lys Asp Ile Met Leu
305     310     315     320
Asn Lys Glu Glu Thr Lys Lys Glu Asn Ser Phe Glu Met Gln Lys Gly
325     330     335
Asp Gln Asn Pro Gln Ile Ala Ala His Val Ile Ser Glu Ala Ser Ser
340     345     350
Lys Thr Thr Ser Val Leu Gln Trp Ala Glu Lys Gly Tyr Thr Met
355     360     365
Ser Asn Asn Leu Val Thr Leu Glu Asn Gly Lys Gln Leu Thr Val Lys
370     375     380
Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr Phe Cys Ser Asn
385     390     395     400
Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser Leu Cys Leu Lys
405     410     415
Ser Pro Gly Arg Phe Glu Arg Ile Leu Arg Ala Ala Asn Thr His
420     425     430

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WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 ser Ser Ala Lys Pro Cys Gly Gln Gln Ser Ile His Leu Gly Gly Val
 435 440 445
 Phe Glu Leu Gln Pro Gly Ala Ser Val Phe Val Asn Val Thr Asp Pro
 450 455 460
 ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe Gly Leu Leu Lys
 465 470 475 480
 Leu Glu

<210> 34
 <211> 422
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MOUSE-HUMAN HYBRID FUSION PROTEIN

<220>
 <221> SITE
 <222> (1)..(266)
 <223> MOUSE ANTI-HUMAN SCFV

<220>
 <221> DOMAIN
 <222> (268)..(421)
 <223> EXTRACELLULAR DOMAIN, SHORT FORM, HUMAN CD154

<400> 34

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1 5 10 15
 Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
 20 25 30
 Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
 35 40 45
 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
 50 55 60
 Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
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 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
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 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
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 Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
 115 120 125
 Asp Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser
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 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
 145 150 155 160
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 165 170 175
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
 180 185 190
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
 195 200 205
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr
 210 215 220
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 225 230 235 240
 Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
 245 250 255
 Gly Thr Gly Thr Thr Val Thr Val Ser Pro Glu Asn Ser Phe Glu
 260 265 270
 Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala His Val Ile Ser
 275 280 285
 Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp Ala Glu Lys Gly
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WO 2005/037989

PCT/US2003/024918

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340 345 350
Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu Arg Ala
355 360 365
Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser Ile His
370 375 380
Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser Val Phe Val Asn
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<210> 35
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<212> DNA
<213> Homo sapiens

<220>
<221> N_region
<222> (1)..(63)
<223> PORTION OF HUMAN IGA HINGE DOMAIN CONTAINING ONLY 1 CYSTEINE

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tgc
63

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Pro Ser Pro Ser Cys
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<212> DNA
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<220>
<221> misc_feature
<222> (1)..(6)
<223> BCLI SITE FOR FUSION TO AMIN TERMINAL SCFVS

<220>
<221> N_region
<222> (8)..(752)
<223> WILD TYPE IGA HINGE, CH2, CH3 DOMAINS
TRUNCATED TO REMOVE SECRETORY COMPONENT ATTACHMENT

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WO 2005/037989

PCT/US2003/024918

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 360
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 420
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 763

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 <212> PRT
 <213> Homo sapiens

<220>
 <221> DOMAIN
 <222> (3)..(250)
 <223> TRUNCATED FORM, REMOVAL OF LAST THREE AMINO ACIDS THAT MEDIATE
 ATTACHMENT TO SECRETORY COMPONENT

<400> 38

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| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Pro | Thr | Pro | Ser | Pro | Ser | Cys | Cys | His | Pro | Arg | Leu | Ser | Leu | His | Arg |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Pro | Ala | Leu | Glu | Asp | Leu | Leu | Leu | Gly | Ser | Glu | Ala | Ile | Leu | Thr | Cys |
| | | 35 | | | | | 40 | | | | | 45 | | | |
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| Pro | Ser | Ser | Gly | Lys | Ser | Ala | Val | Gln | Gly | Pro | Asp | Arg | Asp | Leu | |
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| Cys | Gly | Cys | Tyr | Ser | Val | Ser | Ser | Val | Leu | Pro | Gly | Cys | Ala | Glu | Pro |
| | | | 85 | | | | | 90 | | | | | 95 | | |
| Trp | Asn | His | Gly | Lys | Thr | Phe | Thr | Cys | Thr | Ala | Ala | Tyr | Pro | Glu | Ser |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Lys | Thr | Pro | Leu | Thr | Ala | Thr | Leu | Ser | Lys | Ser | Gly | Asn | Thr | Phe | Arg |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Pro | Glu | Val | His | Leu | Leu | Pro | Pro | Pro | Ser | Glu | Glu | Leu | Ala | Leu | Asn |
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| Glu | Leu | Val | Thr | Leu | Thr | Cys | Leu | Ala | Arg | Gly | Phe | Ser | Pro | Lys | Asp |
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| Val | Leu | Val | Arg | Trp | Leu | Gln | Gly | Ser | Gln | Glu | Leu | Pro | Arg | Glu | Lys |
| | | | 165 | | | | | 170 | | | | | | 175 | |
| Tyr | Leu | Thr | Trp | Ala | Ser | Arg | Gln | Glu | Pro | Ser | Gln | Gly | Thr | Thr | Thr |
| | | | 180 | | | | 185 | | | | | | 190 | | |
| Phe | Ala | Val | Thr | Ser | Ile | Leu | Arg | Val | Ala | Ala | Glu | Asp | Trp | Lys | Lys |
| | | 195 | | | | 200 | | | | | | 205 | | | |
| Gly | Asp | Thr | Phe | Ser | Cys | Met | Val | Gly | His | Glu | Ala | Leu | Pro | Leu | Ala |
| | | 210 | | | | 215 | | | | | 220 | | | | |
| Phe | Thr | Gln | Lys | Thr | Ile | Asp | Arg | Leu | Ala | Gly | Lys | Pro | Thr | His | Val |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 |
| Asn | Val | Ser | Val | Val | Met | Ala | Glu | Val | Asp | | | | | | |

WO 2005/037989

PCT/US2003/024918

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<213> Artificial Sequence

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<210> 40
<211> 4
<212> PRT
<213> Artificial Sequence

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<223> Sequence contained in the core hinge region of
human IgG1.

<400> 40
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<210> 41
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<223> Human IgA-derived hinge.

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Pro Thr Ser Pro Val Pro Gln Asp
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cccggcgagt cgggctcttg aggaaaagaa agtttgccaa ggcacgagta acaagctcac 360
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WO 2005/037989

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<213> Homo sapiens

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Leu Glu Ile Thr Tyr Val Gln Arg Asn Tyr Asp Leu Ser Phe Leu Lys
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Thr Ile Gln Glu Val Ala Gly Tyr Val Leu Ile Ala Leu Asn Thr Val
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Glu Arg Ile Pro Leu Glu Asn Leu Gln Ile Ile Arg Gly Asn Met Tyr
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Tyr Glu Asn Ser Tyr Ala Leu Ala Val Leu Ser Asn Tyr Asp Ala Asn
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Lys Thr Gly Leu Lys Glu Leu Pro Met Arg Asn Leu Gln Glu Ile Leu
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His Gly Ala Val Arg Phe Ser Asn Asn Pro Ala Leu Cys Asn Val Glu
145 150 155 160
Ser Ile Gln Trp Arg Asp Ile Val Ser Ser Asp Phe Leu Ser Asn Met
165 170 175
Ser Met Asp Phe Gln Asn His Leu Gly Ser Cys Gln Lys Cys Asp Pro
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Ser Cys Pro Asn Gly Ser Cys Trp Gly Ala Gly Glu Glu Asn Cys Gln
195 200 205
Lys Leu Thr Lys Ile Ile Cys Ala Gln Gln Cys Ser Gly Arg Cys Arg
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Gly Lys Ser Pro Ser Asp Cys Cys His Asn Gln Cys Ala Ala Gly Cys
225 230 235 240
Thr Gly Pro Arg Glu Ser Asp Cys Leu Val Cys Arg Lys Phe Arg Asp
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Glu Ala Thr Cys Lys Asp Thr Cys Pro Pro Leu Met Leu Tyr Asn Pro
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275 280 285
Ala Thr Cys Val Lys Lys Cys Pro Arg Asn Tyr Val Val Thr Asp His
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Gly Ser Cys Val Arg Ala Cys Gly Ala Asp Ser Tyr Glu Met Glu Glu
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Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp
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Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe Thr His Thr
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Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr Val Lys Glu
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Ile Thr Gly Leu Ser
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WO 2005/037989

PCT/US2003/024918

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<212> DNA
<213> Homo sapiens

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WO 2005/037989

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35 40 45
Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu Leu Thr Tyr
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Leu Pro Thr Asn Ala Ser Leu Ser Phe Leu Gln Asp Ile Gln Glu Val
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Gln Gly Tyr Val Leu Ile Ala His Asn Gln Val Arg Gln Val Pro Leu
85 90 95
Gln Arg Leu Arg Ile Val Arg Gly Thr Gln Leu Phe Glu Asp Asn Tyr
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Ala Leu Ala Val Leu Asp Asn Gly Asp Pro Leu Asn Asn Thr Thr Pro
115 120 125
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130 135 140
Leu Thr Glu Ile Leu Lys Gly Gly Val Leu Ile Gln Arg Asn Pro Gln
145 150 155 160
Leu Cys Tyr Gln Asp Thr Ile Leu Trp Lys Asp Ile Phe His Lys Asn
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Asn Gln Leu Ala Leu Thr Leu Ile Asp Thr Asn Arg Ser Arg Ala Cys
180 185 190
His Pro Cys Ser Pro Met Cys Lys Gly Ser Arg Cys Trp Gly Glu Ser
195 200 205
Ser Glu Asp Cys Gln Ser Leu Thr Arg Thr Val Cys Ala Gly Gly Cys
210 215 220
Ala Arg Cys Lys Gly Pro Leu Pro Thr Asp Cys Cys His Glu Gln Cys
225 230 235 240
Ala Ala Gly Cys Thr Gly Pro Lys His Ser Asp Cys Leu Ala Cys Leu
245 250 255
His Phe Asn His Ser Gly Ile Cys Glu Leu His Cys Pro Ala Leu Val
260 265 270
Thr Tyr Asn Thr Asp Thr Phe Glu Ser Met Pro Asn Pro Glu Gly Arg
275 280 285
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Ser Thr Asp Val Gly Ser Cys Thr Leu Val Cys Pro Leu His Asn Gln
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Glu Val Thr Ala Glu Asp Gly Thr Gln Arg Cys Glu Lys Cys Ser Lys
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Val Arg Ala Val Thr Ser Ala Asn Ile Gln Glu Phe Ala Gly Cys Lys
355 360 365
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WO 2005/037989

PCT/US2003/024918

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WO 2005/037989

PCT/US2003/024918

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WO 2005/037989

PCT/US2003/024918

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WO 2005/037989

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WO 2005/037989

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Page 37

WO 2005/037989

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Asp Gly Val Arg Lys Cys Lys Lys Cys Glu Gly Pro Cys Arg Lys Val
325 330 335
Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn
340 345 350
Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp
355 360 365
Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe Thr His Thr
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385 390 395 400
Ile Thr Gly Leu Ser
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WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

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WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

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| atcagcgag | ctactgccat | ccaatcgaga | ccctggtgga | catcttccag | gagtaccctg | 900 |
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| aatcaccgag | cccgggaagat | tagagagttt | tatttctggg | attcctgtag | acacaccac | 1620 |
| ccacatacat | acattttatat | atatatatata | tatatata | taaaaataaa | tatctctatt | 1680 |
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| | | 35 | | | | 40 | | | | | 45 | | | | |
| Arg | Ser | Tyr | Cys | His | Pro | Ile | Glu | Thr | Leu | Val | Asp | Ile | Phe | Gln | Glu |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Tyr | Pro | Asp | Glu | Ile | Glu | Tyr | Ile | Phe | Lys | Pro | Ser | Cys | Val | Pro | Leu |
| | 65 | | | | 70 | | | | 75 | | | | 80 | | |
| Met | Arg | Cys | Gly | Gly | Cys | Ser | Asn | Asp | Glu | Gly | Leu | Glu | Cys | Val | Pro |
| | | | 85 | | | | | 90 | | | | | 95 | | |
| Thr | Glu | Glu | Ser | Asn | Ile | Thr | Met | Gln | Ile | Met | Arg | Ile | Lys | Pro | His |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Gln | Gly | Gln | His | Ile | Gly | Glu | Met | Ser | Phe | Leu | Gln | His | Asn | Lys | Cys |
| | | 115 | | | | 120 | | | | | | 125 | | | |
| Glu | Cys | Arg | Pro | Lys | Lys | Asp | Arg | Ala | Arg | Gln | Glu | Asn | Pro | Cys | Gly |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Pro | Cys | Ser | Glu | Arg | Arg | Lys | His | Leu | Phe | Val | Gln | Asp | Pro | Gln | Thr |
| | 145 | | | | 150 | | | | | 155 | | | | 160 | |
| Cys | Lys | Cys | Ser | Cys | Lys | Asn | Thr | His | Ser | Arg | Cys | Lys | Ala | Arg | Gln |

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

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180 185 190

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35 40 45
Gly Pro Glu Thr Leu Cys Gly Ala Glu Leu Val Asp Ala Leu Gln Phe
50 55 60
Val Cys Gly Asp Arg Gly Phe Tyr Phe Asn Lys Pro Thr Gly Tyr Gly
65 70 75 80
Ser Ser Ser Arg Arg Ala Pro Gln Thr Gly Ile Val Asp Glu Cys Cys
85 90 95
Phe Arg Ser Cys Asp Leu Arg Arg Leu Glu Met Tyr Cys Ala Pro Leu
100 105 110
Lys Pro Ala Lys Ser Ala Arg Ser Val Arg Ala Gln Arg His Thr Asp
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Ser Ala Gly Asn Lys Asn Tyr Arg Met
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WO 2005/037989

PCT/US2003/024918

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WO 2005/037989

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WO 2005/037989

PCT/US2003/024918

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WO 2005/037989

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WO 2005/037989

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WO 2005/037989

PCT/US2003/024918

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WO 2005/037989

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WO 2005/037989

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PCT/US2003/024918

Page 52

WO 2005/037989

PCT/US2003/024918

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WO 2005/037989

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WO 2005/037989

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WO 2005/037989

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WO 2005/037989

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WO 2005/037989

PCT/US2003/024918

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<211> 630
<212> PRT
<213> Mus musculus

<400> 69
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Ser Ser Gln Asp Thr Ser Ser Ser Ala Ser Thr Thr Thr Pro Val
35 40 45
His Ser Ser Asn Ser Asp Pro Ala Thr Arg Pro Pro Gly Asp Ser Thr
50 55 60
Ser Ser Pro Val Gln Ser Ser Thr Ser Ser Pro Ala Thr Arg Ala Pro
65 70 75 80
Glu Asp Ser Thr Ser Thr Ala Val Leu Ser Gly Thr Ser Ser Pro Ala
85 90 95
Thr Thr Ala Pro Val Asn Ser Ala Ser Pro Val Ala His Gly Asp
100 105 110
Thr Ser Ser Pro Ala Thr Ser Pro Leu Lys Asp Ser Asn Ser Ser Pro
115 120 125
Val Val His Ser Gly Thr Ser Ala Ala Thr Thr Ala Pro Val Asp
130 135 140
Ser Thr Ser Ser Pro Val Val His Gly Gly Thr Ser Ser Pro Ala Thr
145 150 155 160
Ser Pro Pro Gly Asp Ser Thr Ser Ser Pro Asp His Ser Ser Thr
165 170 175 180
Ser Pro Ala Thr Arg Ala Pro Glu Asp Ser Thr Ser Thr Ala Val Leu
185 190 195
Ser Gly Thr Ser Ser Pro Ala Thr Thr Ala Pro Val Asp Ser Thr Ser
200 205 210
Ser Pro Val Ala His Asp Asp Thr Ser Ser Pro Ala Thr Ser Leu Ser
215 220 225
Glu Asp Ser Ala Ser Ser Pro Val Ala His Gly Gly Thr Ser Ser Pro
230 235 240
Ala Thr Ser Pro Leu Arg Asp Ser Thr Ser Ser Pro Val His Ser
245 250 255
Ala Ser Ile Gln Asn Ile Lys Thr Thr Ser Asp Leu Ala Ser Thr Pro
260 265 270
Asp His Asn Gly Thr Ser Val Thr Thr Thr Ser Ser Ala Leu Gly Ser
275 280 285
Ala Thr Ser Pro Asp His Ser Gly Thr Ser Thr Thr Thr Asn Ser Ser
290 295 300
Glu Ser Val Leu Ala Thr Thr Pro Val Tyr Ser Ser Met Pro Phe Ser
305 310 315 320
Thr Thr Lys Val Thr Ser Gly Ser Ala Ile Ile Pro Asp His Asn Gly
325 330 335
Ser Ser Val Leu Pro Thr Ser Ser Val Leu Gly Ser Ala Thr Ser Leu
340 345 350
Val Tyr Asn Thr Ser Ala Ile Ala Thr Thr Pro Val Ser Asn Gly Thr
355 360 365
Gln Pro Ser Val Pro Ser Gln Tyr Pro Val Ser Pro Thr Met Ala Thr
370 375 380
Thr Ser Ser His Ser Thr Ile Ala Ser Ser Ser Tyr Ser Thr Val
385 390 395 400
Pro Phe Ser Thr Phe Ser Ser Asn Ser Ser Pro Gln Leu Ser Val Gly
405 410 415
Val Ser Phe Phe Phe Leu Phe Phe Tyr Ile Gln Asn His Pro Phe Asn
420 425 430
Ser Ser Leu Glu Asp Pro Ser Ser Asn Tyr Tyr Gln Glu Leu Lys Arg
435 440 445
Asn Ile Ser Gly Leu Phe Leu Gln Ile Phe Asn Gly Asp Phe Leu Gly
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WO 2005/037989

PCT/US2003/024918

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485 490 495
Leu Ile Gln His Lys Lys Glu Ala Asp Ser Tyr Asn Leu Thr Ile Ser
500 505 510
Glu Val Lys Val Asn Glu Met Gln Phe Pro Pro Ser Ala Gln Ser Arg
515 520 525
Pro Gly Val Pro Gly Trp Gly Ile Ala Leu Leu Val Leu Val Cys Ile
530 535 540
Leu Val Ala Leu Ala Ile Val Tyr Phe Leu Ala Leu Ala Val Cys Gln
545 550 555 560
Cys Arg Arg Lys Ser Tyr Gly Gln Leu Asp Ile Phe Pro Thr Gln Asp
565 570 575
Thr Tyr His Pro Met Ser Glu Tyr Pro Thr Tyr His Thr His Gly Arg
580 585 590
Tyr Val Pro Pro Gly Ser Thr Lys Arg Gln Pro Tyr Glu Glu Val Ser
595 600 605
Ala Gly Asn Gly Ser Ser Ser Leu Ser Tyr Thr Asn Pro Ala Val Val
610 615 620
Thr Thr Ser Ala Asn Leu
625 630

<210> 70
<211> 755
<212> DNA
<213> Homo sapiens

<400> 70
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aaggccgggg cacagggggt tcgacgggag atgctgatgg cccaggaggc cctggcattc 120
ctgatggccc agggggcaat gctggcggcc caggagaggc ggggtgccacg ggcggcagag 180
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cgcatggcgg cgcggcttca gggctgaatg gatgctgcag atgcggggcc agggggccgg 300
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<210> 71
<211> 180
<212> PRT
<213> Homo sapiens

<400> 71
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Gly Pro Gly Gly Pro Gly Ile Pro Asp Gly Pro Gly Gly Asn Ala Gly
20 25 30
Gly Pro Gly Glu Ala Gly Ala Thr Gly Gly Arg Gly Pro Arg Gly Ala
35 40 45
Gly Ala Ala Arg Ala Ser Gly Pro Gly Gly Gly Ala Pro Arg Gly Pro
50 55 60
His Gly Gly Ala Ala Ser Gly Leu Asn Gly Cys Cys Arg Cys Gly Ala
65 70 75 80
Arg Gly Pro Glu Ser Arg Leu Leu Glu Phe Tyr Leu Ala Met Pro Phe
85 90 95
Ala Thr Pro Met Glu Ala Glu Leu Ala Arg Arg Ser Leu Ala Gln Asp
100 105 110
Ala Pro Pro Leu Pro Val Pro Gly Val Leu Leu Lys Glu Phe Thr Val
115 120 125
Ser Gly Asn Ile Leu Thr Ile Arg Leu Thr Ala Ala Asp His Arg Gln
130 135 140
Leu Gln Leu Ser Ile Ser Ser Cys Leu Gln Gln Leu Ser Leu Leu Met

WO 2005/037989

PCT/US2003/024918

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Gly Gln Arg Arg
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<210> 72
<211> 1524
<212> DNA
<213> Homo sapiens

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cggtgaaga ggccgctggg atcggcatcc tgacagtgat cctgggagtc ttactgtcta 180
tcggctgttg gtattgtaga agacgaaatg gatacagagc cttgatggat aaaagtcttc 240
atgttggcac tcaatgtgcc ttaacaagaa gatgcccaca agaagggttt gatcatcggg 300
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gtaattgttag taaatccatg gtgttatttt ctgagagaca gaattcaagt ggggtattctg 720
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<210> 73
<211> 118
<212> PRT
<213> Homo sapiens

<400> 73
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His Gly His Ser Tyr Thr Thr Ala Glu Glu Ala Ala Gly Ile Gly Ile
20 25 30
Leu Thr Val Ile Leu Gly Val Leu Leu Ile Gly Cys Trp Tyr Cys
35 40 45
Arg Arg Arg Asn Gly Tyr Arg Ala Leu Met Asp Lys Ser Leu His Val
50 55 60
Gly Thr Gln Cys Ala Leu Thr Arg Arg Cys Pro Gln Glu Gly Phe Asp
65 70 75 80
His Arg Asp Ser Lys Val Ser Leu Gln Glu Lys Asn Cys Glu Pro Val
85 90 95
Val Pro Asn Ala Pro Pro Ala Tyr Glu Lys Leu Ser Ala Glu Gln Ser
100 105 110
Pro Pro Pro Tyr Ser Pro
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<210> 74
<211> 1602
<212> DNA
<213> Mus musculus

WO 2005/037989

PCT/US2003/024918

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cttcagaaga agaagaagaa gaagcaacc caggaggaaa ggcagccact cctcatggac 1560
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<210> 75
<211> 533
<212> PRT
<213> Mus musculus
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20 25 30
Lys Glu Cys Cys Pro Pro Trp Ile Gly Asp Gly Ser Pro Cys Gly Gln
35 40 45
Leu Ser Gly Arg Gly Ser Cys Gln Asp Ile Leu Leu Ser Ser Ala Pro
50 55 60
Ser Gly Pro Gln Phe Pro Phe Lys Gly Val Asp Asp Arg Glu Ser Trp
65 70 75 80
Pro Ser Val Phe Tyr Asn Arg Thr Cys Gln Cys Ser Gly Asn Phe Met
85 90 95
Gly Phe Asn Cys Gly Asn Cys Lys Phe Gly Phe Gly Gly Pro Asn Cys
100 105 110
Thr Glu Lys Arg Val Leu Ile Arg Asn Ile Phe Asp Leu Ser Val
115 120 125
Ser Glu Lys Asn Lys Phe Phe Ser Tyr Leu Thr Leu Ala Lys His Thr
130 135 140
Ile Ser Ser Val Tyr Val Ile Pro Thr Gly Thr Tyr Gly Gln Met Asn
145 150 155 160
Asn Gly Ser Thr Pro Met Phe Asn Asp Ile Asn Ile Tyr Asp Leu Phe
165 170 175
Val Trp Met His Tyr Tyr Val Ser Arg Asp Thr Leu Leu Gly Ser
180 185 190
Glu Ile Trp Arg Gln Ile Asp Phe Ala His Glu Ala Pro Gly Phe Leu
195 200 205
Pro Trp His Arg Leu Phe Leu Leu Trp Glu Gln Glu Ile Arg Glu
210 215 220
Leu Thr Gly Asp Glu Asn Phe Thr Val Pro Tyr Trp Asp Trp Arg Asp
225 230 235 240
Ala Glu Asn Cys Asp Ile Cys Thr Asp Glu Tyr Leu Gly Gly Arg His
245 250 255
Pro Glu Asn Pro Asn Leu Leu Ser Pro Ala Ser Phe Phe Ser Ser Trp
260 265 270
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WO 2005/037989

PCT/US2003/024918

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 305 310 315 320
 Cys Leu Ser Leu Thr Gln Tyr Glu Ser Gly Ser Met Asp Arg Thr Ala
 325 330 335
 Asn Phe Ser Phe Arg Asn Thr Leu Glu Gly Phe Ala Ser Pro Leu Thr
 340 345 350
 Gly Ile Ala Asp Pro Ser Gln Ser Met His Asn Ala Leu His Ile
 355 360 365
 Phe Met Asn Gly Thr Met Ser Gln Val Gln Gly Ser Ala Asn Asp Pro
 370 375 380
 Ile Phe Leu Leu His His Ala Phe Val Asp Ser Ile Phe Glu Gln Trp
 385 390 395 400
 Leu Arg Arg His Arg Pro Leu Leu Glu Val Tyr Pro Glu Ala Asn Ala
 405 410 415
 Pro Ile Gly Arg Asn Arg Asp Ser Tyr Met Val Pro Phe Ile Pro Leu
 420 425 430
 Tyr Arg Asn Gly Asp Phe Phe Ile Thr Ser Lys Asp Leu Gly Tyr Asp
 435 440 445
 Tyr Ser Tyr Leu Gln Glu Ser Asp Pro Gly Phe Tyr Arg Asn Tyr Ile
 450 455 460
 Glu Pro Tyr Leu Glu Gln Ala Ser Arg Ile Trp Pro Trp Leu Leu Gly
 465 470 475 480
 Ala Ala Leu Val Gly Ala Val Ile Ala Ala Leu Ser Gly Leu Ser
 485 490 495
 Ser Arg Leu Cys Leu Gln Lys Lys Lys Lys Lys Gln Pro Gln Glu
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 Glu Arg Gln Pro Leu Leu Met Asp Lys Asp Asp Tyr His Ser Leu Leu
 515 520 525
 Tyr Gln Ser His Leu
 530

<210> 76
 <211> 2130
 <212> DNA
 <213> Homo sapiens

<400> 76
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 gaaagtgccg agatcctgca ggctgtgccg tccggtgagg gggatgcatt tgagctgact 1560
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WO 2005/037989

PCT/US2003/024918

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<211> 661
<212> PRT
<213> Homo sapiens

<400> 77
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35 40 45
Tyr Pro Glu Trp Thr Glu Ala Gln Arg Leu Asp Cys Trp Arg Gly Gly
50 55 60
Gln Val Ser Leu Lys Val Ser Asn Asp Gly Pro Thr Leu Ile Gly Ala
65 70 75 80
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WO 2005/037989

PCT/US2003/024918

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WO 2005/037989

PCT/US2003/024918

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WO 2005/037989

PCT/US2003/024918

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WO 2005/037989

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1060 1065 1070
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1075 1080 1085
Ala Met Leu Lys Asn Thr Val Pro Ile Thr Phe Pro Ser Ser Tyr Lys
1090 1095 1100
Asp Ala Leu Lys Asp Val Glu Glu Arg Ala Gln Ala Ile Ile Asp Thr
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WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

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Ala Gly Gln Gly Pro Lys Pro Glu Ala Asp Ser Gln Glu Gln Gly His
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Pro Gln Thr Gly Cys Glu Cys Glu Asp Gly Pro Asp Gly Gln Glu Met
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Asp Pro Pro Asn Pro Glu Glu Val Lys Thr Pro Glu Glu Glu Met Arg
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WO 2005/037989

PCT/US2003/024918

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WO 2005/037989

PCT/US2003/024918

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PCT/US2003/024918

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WO 2005/037989

PCT/US2003/024918

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<210> 89
<211> 782
<212> PRT

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
<213> Homo sapiens

<400> 89

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 20      25      30
Ala Tyr Lys Gln Gln Ser Leu Leu His Pro Asp Lys Gly Gly Ser
 35      40      45
His Ala Leu Met Gln Glu Leu Asn Ser Leu Trp Gly Thr Phe Lys Thr
 50      55      60
Glu Val Tyr Asn Leu Arg Met Asn Leu Gly Gly Thr Gly Phe Gln Gly
 65      70      75      80
Ser Pro Pro Arg Thr Ala Glu Arg Gly Thr Glu Glu Ser Gly His Ser
 85      90      95
Pro Leu His Asp Asp Tyr Trp Ser Phe Ser Tyr Gly Ser Lys Tyr Phe
100      105      110
Thr Arg Glu Trp Asn Asp Phe Phe Arg Lys Trp Asp Pro Ser Tyr Gln
115      120      125
Ser Pro Pro Lys Thr Ala Glu Ser Ser Glu Gln Pro Asp Leu Phe Cys
130      135      140
Tyr Glu Glu Pro Leu Leu Ser Pro Asn Pro Ser Ser Pro Thr Asp Thr
145      150      155      160
Pro Ala His Thr Ala Gly Arg Arg Arg Asn Pro Cys Val Ala Glu Pro
165      170      175
Asp Asp Ser Ile Ser Pro Asp Pro Pro Arg Thr Pro Val Ser Arg Lys
180      185      190      195
Arg Pro Arg Pro Ala Gly Ala Thr Gly Gly Gly Gly Gly Val His
195      200      205      210
Ala Asn Gly Gly Ser Val Phe Gly His Pro Thr Gly Gly Thr Ser Thr
210      215      220
Pro Ala His Pro Pro Pro Tyr His Ser Gln Gly Gly Ser Glu Ser Met
225      230      235      240
Gly Gly Ser Asp Ser Ser Gly Phe Ala Glu Gly Ser Phe Arg Ser Asp
245      250      255
Pro Arg Cys Glu Ser Glu Asn Glu Ser Tyr Ser Gln Ser Cys Ser Gln
260      265      270
Ser Ser Phe Asn Ala Thr Pro Pro Lys Lys Ala Arg Glu Asp Pro Ala
275      280      285
Pro Ser Asp Phe Pro Ser Ser Leu Thr Gly Tyr Leu Ser His Ala Ile
290      295      300
Tyr Ser Asn Lys Thr Phe Pro Ala Phe Leu Val Tyr Ser Thr Lys Glu
305      310      315      320
Lys Cys Lys Gln Leu Tyr Asp Thr Ile Gly Lys Phe Arg Pro Glu Phe
325      330      335
Lys Cys Leu Val His Tyr Glu Glu Gly Gly Met Leu Phe Phe Leu Thr
340      345      350
Met Thr Lys His Arg Val Ser Ala Val Lys Asn Tyr Cys Ser Lys Leu
355      360      365
Cys Ser Val Ser Phe Leu Met Cys Lys Ala Val Thr Lys Pro Met Glu
370      375      380
Cys Tyr Gln Val Val Thr Ala Ala Pro Phe Gln Leu Ile Thr Glu Asn
385      390      395      400
Lys Pro Gly Leu His Gln Phe Glu Phe Thr Asp Glu Pro Glu Glu Gln
405      410      415
Lys Ala Val Asp Trp Ile Met Val Ala Asp Phe Ala Leu Glu Asn Asn
420      425      430
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435      440      445
Glu Val Pro Ser Cys Ile Lys Cys Ser Lys Glu Glu Thr Arg Leu Gln
450      455      460
Ile His Trp Lys Asn His Arg Lys His Ala Glu Asn Ala Asp Leu Phe
465      470      475      480
Leu Asn Cys Lys Ala Gln Lys Thr Ile Cys Gln Gln Ala Ala Asp Gly
485      490      495
Val Leu Ala Ser Arg Arg Leu Lys Leu Val Glu Cys Thr Arg Ser Gln
500      505      510
Leu Leu Lys Glu Arg Leu Gln Gln Ser Leu Leu Arg Leu Lys Glu Leu
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WO 2005/037989

PCT/US2003/024918

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 545 550 555 560
 Leu Thr Glu Asn Val Pro Lys Arg Arg Asn Ile Leu Phe Arg Gly Pro
 565 570 575
 Val Asn Ser Gly Lys Thr Gly Leu Ala Ala Leu Ile Ser Leu Leu
 580 585 590
 Gly Gly Lys Ser Leu Asn Ile Asn Cys Pro Ala Asp Lys Leu Ala Phe
 595 600 605
 Glu Leu Gly Val Ala Gln Asp Gln Phe Val Val Cys Phe Glu Asp Val
 610 615 620
 Lys Gly Gln Ile Ala Leu Asn Lys Gln Leu Gln Pro Gly Met Gly Val
 625 630 635 640
 Ala Asn Leu Asp Asn Leu Arg Asp Tyr Leu Asp Gly Ser Val Lys Val
 645 650 655
 Asn Leu Glu Lys Lys His Ser Asn Lys Arg Ser Gln Leu Phe Pro Pro
 660 665 670
 Cys Val Cys Thr Met Asn Glu Tyr Leu Leu Pro Gln Thr Val Trp Ala
 675 680 685
 Arg Phe His Met Val Leu Asp Phe Thr Cys Lys Pro His Leu Ala Gln
 690 695 700
 Ser Leu Glu Lys Cys Glu Phe Leu Gln Arg Glu Arg Ile Ile Gln Ser
 705 710 715 720
 Gly Asp Thr Leu Ala Leu Leu Leu Ile Trp Asn Phe Thr Ser Asp Val
 725 730 735
 Phe Asp Pro Asp Ile Gln Gly Leu Val Lys Glu Val Arg Asp Gln Phe
 740 745 750
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 Gln Glu Gly Asp Asp Pro Leu Lys Asp Ile Cys Glu Tyr Ser
 770 775 780

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 <211> 1504
 <212> DNA
 <213> Homo sapiens

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 caggacatca acttggacat tcctagtttt caaatgagtg atgatatga cगतataaaa 180
 tgggaaaaaa cttcagacaa gaaaaagatt gcacaattca gaaaagagaa agagactttc 240
 aaggaaaaag atacatataa gctattttaa attggaactc tgaaaattaa gcatctgaag 300
 accgatgatc aggatattca caaggtatca atatatgata caaaaggaaa aaatgtgttg 360
 gaaaaaatat ttgatttgaa gattcaagag aggggtctca aaccaaatat ctcttgact 420
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 tatcaagatg ggaacatctt aaaactttct cagaggggtc tcacacacaa gtggaccacc 540
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 gagcctgtca gctgtccaga gaaagggtctg gacatctatc tcattcattgg catatgtgga 660
 ggaggcagcc tcttgatggg ctttgtggca ctgctcgttt tctatatcac caaaaggaaa 720
 aaacagagga gtcggagaaa tgaatgaggag ctggagacaa gagcccacag agtagctact 780
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 ttttcaataa aaagcactgt ggatttctgc cctctgatg tgcataatcc tacttccatg 1140
 aggtgttttc tgtgtgcaga acattgtcac ctctgaggc tctgtggcc agccacctct 1200
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<210> 91
 <211> 351

WO 2005/037989

PCT/US2003/024918

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<212> PRT

<213> Homo sapiens

<400> 91

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Thr Trp Gly Ala Leu Gly Gln Asp Ile Asn Leu Asp Ile Pro Ser Phe
 35      40      45
Gln Met Ser Asp Asp Ile Asp Asp Ile Lys Trp Glu Lys Thr Ser Asp
 50      55      60
Lys Lys Lys Ile Ala Gln Phe Arg Lys Glu Lys Glu Thr Phe Lys Glu
 65      70      75      80
Lys Asp Thr Tyr Lys Leu Phe Lys Asn Gly Thr Leu Lys Ile Lys His
 85      90      95
Leu Lys Thr Asp Asp Gln Asp Ile Tyr Lys Val Ser Ile Tyr Asp Thr
 100      105      110
Lys Gly Lys Asn Val Leu Glu Lys Ile Phe Asp Leu Lys Ile Gln Glu
 115      120      125
Arg Val Ser Lys Pro Lys Ile Ser Trp Thr Cys Ile Asn Thr Thr Leu
 130      135      140
Thr Cys Glu Val Met Asn Gly Thr Asp Pro Glu Leu Asn Leu Tyr Gln
 145      150      155      160
Asp Gly Lys His Leu Lys Leu Ser Gln Arg Val Ile Thr His Lys Trp
 165      170      175
Thr Thr Ser Leu Ser Ala Lys Phe Lys Cys Thr Ala Gly Asn Lys Val
 180      185      190
Ser Lys Glu Ser Ser Val Glu Pro Val Ser Cys Pro Glu Lys Gly Leu
 195      200      205
Asp Ile Tyr Leu Ile Ile Gly Ile Cys Gly Gly Gly Ser Leu Leu Met
 210      215      220
Val Phe Val Ala Leu Leu Val Phe Tyr Ile Thr Lys Arg Lys Lys Gln
 225      230      235      240
Arg Ser Arg Arg Asn Asp Glu Glu Leu Glu Thr Arg Ala His Arg Val
 245      250      255
Ala Thr Glu Glu Arg Gly Arg Lys Pro Gln Gln Ile Pro Ala Ser Thr
 260      265      270
Pro Gln Asn Pro Ala Thr Ser Gln His Pro Pro Pro Pro Gly His
 275      280      285
Arg Ser Gln Ala Pro Ser His Arg Pro Pro Pro Pro Gly His Arg Val
 290      295      300
Gln His Gln Pro Gln Lys Arg Pro Pro Ala Pro Ser Gly Thr Gln Val
 305      310      315      320
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<210> 92

<211> 2026

<212> DNA

<213> Homo sapiens

<400> 92

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agtcaacatg gagatctctc tctctctaca cacacacaca cacacacaca cacacacaca 180
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tggttttgcc aggaggaagt tgacagtcca acttcaaaca tgggtgacgc agggcccaca 660
ctgcctgctc cccgtccccc cctccctga gcacgccacc ccgccccttc cctctctgag 720
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WO 2005/037989

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aaggaaggag ttcccagttt tacccaaggc tgactctggg atccacatgt cagccctctg 960
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gagtctctgg ccatgtgtgt gagtactgtg tgtaggggaa tgtgtgagtc tgtgtgtgag 1980
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<210> 93
<211> 495
<212> PRT
<213> Homo sapiens

<400> 93

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Met | Gly | Ser | Leu | Gln | Pro | Leu | Ala | Thr | Leu | Tyr | Leu | Leu | Gly |
| 1 | | | 5 | | | | | | 10 | | | | | 15 | |
| Met | Leu | Val | Ala | Ser | Cys | Leu | Gly | Arg | Leu | Ser | Trp | Tyr | Asp | Pro | Asp |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Phe | Gln | Ala | Arg | Leu | Thr | Arg | Ser | Asn | Ser | Lys | Cys | Gln | Gly | Gln | Leu |
| | | 35 | | | | 40 | | | | | 45 | | | | |
| Glu | Val | Tyr | Leu | Lys | Asp | Gly | Trp | His | Met | Val | Cys | Ser | Gln | Ser | Trp |
| | 50 | | | | 55 | | | | | | 60 | | | | |
| Gly | Arg | Ser | Ser | Lys | Gln | Trp | Glu | Asp | Pro | Ser | Gln | Ala | Ser | Lys | Val |
| 65 | | | | 70 | | | | 75 | | | | | | 80 | |
| Cys | Gln | Arg | Leu | Asn | Cys | Gly | Val | Pro | Leu | Ser | Leu | Gly | Pro | Phe | Leu |
| | | | 85 | | | | | 90 | | | | | 95 | | |
| Val | Thr | Tyr | Thr | Pro | Gln | Ser | Ser | Ile | Ile | Cys | Tyr | Gly | Gln | Leu | Gly |
| | 100 | | | | | | | 105 | | | | | 110 | | |
| Ser | Phe | Ser | Asn | Cys | Ser | His | Ser | Arg | Asn | Asp | Met | Cys | His | Ser | Leu |
| | 115 | | | | | 120 | | | | | | 125 | | | |
| Gly | Leu | Thr | Cys | Leu | Glu | Pro | Gln | Lys | Thr | Thr | Pro | Pro | Thr | Thr | Arg |
| | 130 | | | | 135 | | | | | | 140 | | | | |
| Pro | Pro | Pro | Thr | Thr | Thr | Pro | Glu | Pro | Thr | Ala | Pro | Pro | Arg | Leu | Gln |
| 145 | | | | 150 | | | | | | 155 | | | | 160 | |
| Leu | Val | Ala | Gln | Ser | Gly | Gly | Gln | His | Cys | Ala | Gly | Val | Val | Glu | Phe |
| | | | 165 | | | | | 170 | | | | | | 175 | |
| Tyr | Ser | Gly | Ser | Leu | Gly | Gly | Thr | Ile | Ser | Tyr | Glu | Ala | Gln | Asp | Lys |
| | 180 | | | | | | 185 | | | | | | 190 | | |
| Thr | Gln | Asp | Leu | Glu | Asn | Phe | Leu | Cys | Asn | Asn | Leu | Gln | Cys | Gly | Ser |
| | 195 | | | | | 200 | | | | | 205 | | | | |
| Phe | Leu | Lys | His | Leu | Pro | Glu | Thr | Glu | Ala | Gly | Arg | Ala | Gln | Asp | Pro |
| | 210 | | | | 215 | | | | | | 220 | | | | |
| Gly | Glu | Pro | Arg | Glu | His | Gln | Pro | Leu | Pro | Ile | Gln | Trp | Lys | Ile | Gln |
| 225 | | | | 230 | | | | | | 235 | | | | 240 | |
| Asn | Ser | Ser | Cys | Thr | Ser | Leu | Glu | His | Cys | Phe | Arg | Lys | Ile | Lys | Pro |
| | | | 245 | | | | | 250 | | | | | 255 | | |
| Gln | Lys | Ser | Gly | Arg | Val | Leu | Ala | Leu | Leu | Cys | Ser | Gly | Phe | Gln | Pro |
| | | | 260 | | | | 265 | | | | | | 270 | | |
| Lys | Val | Gln | Ser | Arg | Leu | Val | Gly | Ser | Ser | Ile | Cys | Glu | Gly | Thr | |
| | 275 | | | | | 280 | | | | | 285 | | | | |
| Val | Glu | Val | Arg | Gln | Gly | Ala | Gln | Trp | Ala | Ala | Leu | Cys | Asp | Ser | Ser |
| | 290 | | | | 295 | | | | | | 300 | | | | |
| Ser | Ala | Arg | Ser | Ser | Leu | Arg | Trp | Glu | Glu | Val | Cys | Arg | Glu | Gln | Gln |
| 305 | | | | 310 | | | | | | 315 | | | | 320 | |
| Cys | Gly | Ser | Val | Asn | Ser | Tyr | Arg | Val | Leu | Asp | Ala | Gly | Asp | Pro | Thr |

WO 2005/037989

PCT/US2003/024918

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 355 360 365
 Asp Pro Asn Pro Ala Gly Leu Ala Ala Gly Thr Val Ala Ser Ile Ile
 370 375 380
 Leu Ala Leu Val Leu Leu Val Val Leu Leu Val Val Cys Gly Pro Leu
 385 390 395 400
 Ala Tyr Lys Lys Leu Val Lys Lys Phe Arg Gln Lys Lys Gln Arg Gln
 405 410 415
 Trp Ile Gly Pro Thr Gly Met Asn Gln Asn Met Ser Phe His Arg Asn
 420 425 430
 His Thr Ala Thr Val Arg Ser His Ala Glu Asn Pro Thr Ala Ser His
 435 440 445
 Val Asp Asn Glu Tyr Ser Gln Pro Pro Arg Asn Ser Arg Leu Ser Ala
 450 455 460
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 465 470 475 480
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 485 490 495

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 <211> 1586
 <212> DNA
 <213> Homo sapiens

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 ccagatactg gactttatta tgatgaatat ctcaagcaag tgattgatgt gctggaaaaca 420
 gataaacact tcagagaaaa gctccagaaa gcagacatag aggaaataaa gagtgggagg 480
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 <212> PRT
 <213> Homo sapiens

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 Lys Val Gln Asn Ile His Pro Val Glu Ser Ala Lys Ile Glu Pro Pro
 35 40 45

WO 2005/037989

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 85 90 95
 His His Val Arg Thr Lys Leu Asp Glu Leu Lys Arg Gln Glu Val Gly
 100 105 110
 Arg Leu Arg Met Leu Ile Lys Ala Lys Leu Asp Ser Leu Gln Asp Ile
 115 120 125
 Gly Met Asp His Gln Ala Leu Leu Lys Gln Phe Asp His Leu Asn His
 130 135 140
 Leu Asn Pro Asp Lys Phe Glu Ser Thr Asp Leu Asp Met Leu Ile Lys
 145 150 155 160
 Ala Ala Thr Ser Asp Leu Glu His Tyr Asp Lys Thr Arg His Glu Glu
 165 170 175
 Phe Lys Lys Tyr Glu Met Met Lys Glu His Glu Arg Arg Glu Tyr Leu
 180 185 190
 Lys Thr Leu Asn Glu Glu Lys Arg Lys Glu Glu Glu Ser Lys Phe Glu
 195 200 205
 Glu Met Lys Lys Lys His Glu Asn His Pro Lys Val Asn His Pro Gly
 210 215 220
 Ser Lys Asp Gln Leu Lys Glu Val Trp Glu Glu Thr Asp Gly Leu Asp
 225 230 235 240
 Pro Asn Asp Phe Asp Pro Lys Thr Phe Phe Lys Leu His Asp Val Asn
 245 250 255
 Ser Asp Gly Phe Leu Asp Glu Gln Glu Leu Glu Ala Leu Phe Thr Lys
 260 265 270
 Glu Leu Glu Lys Val Tyr Asp Pro Lys Asn Glu Glu Asp Asp Met Val
 275 280 285
 Glu Met Glu Glu Glu Arg Leu Arg Met Arg Glu His Val Met Asn Glu
 290 295 300
 Val Asp Thr Asn Lys Asp Arg Leu Val Thr Leu Glu Glu Phe Leu Lys
 305 310 315 320
 Ala Thr Glu Lys Lys Glu Phe Leu Glu Pro Asp Ser Trp Glu Thr Leu
 325 330 335
 Asp Gln Gln Gln Phe Phe Thr Glu Glu Glu Leu Lys Glu Tyr Glu Asn
 340 345 350
 Ile Ile Ala Leu Gln Glu Asn Glu Leu Lys Lys Lys Ala Asp Glu Leu
 355 360 365
 Gln Lys Gln Lys Glu Glu Leu Gln Arg Gln His Asp Gln Leu Glu Ala
 370 375 380
 Gln Lys Leu Glu Tyr His Gln Val Ile Gln Gln Met Glu Gln Lys Lys
 385 390 395 400
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 405 410 415
 Glu Pro His Ile
 420

<210> 96
 <211> 1204
 <212> DNA
 <213> Homo sapiens

<400> 96
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 cagcaactgg gcacagaaag gagccgcctg ggcagggacc atggcacggc cacatccctg 120
 gtggctgtgc gttctgggga ccttggtggg gctctcagct actccagccc ccaagagctg 180
 cccagagagg cactactggg ctcaaggaaa gctgtgctgc cagatgtgtg agccaggaac 240
 attcctcgtg aaggactgtg accagcatag aaaggctgct cagtgtgata cttgcatacc 300
 gggggtctcc ttctctcctg accaccacac ccggcccccac tgtgagagct gtcggcactg 360
 taactctggt cttctcgttc gcaactgcac catcactgcc aatgctgagt gtgcctgtcg 420
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 gcagctgcct gcccggaact tctctaccca ctggccaccc caaagatccc tgtgcagctc 660
 cgatctttatt cgatccttg tgatcttctc tggaatgttc cttgttttca ccctggccgg 720
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WO 2005/037989

PCT/US2003/024918

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tggcagccac aactgcagtc ccacccctctt gtcaggggccc ttctctgtgt acacgtgaca 1020
gagtgccctt tcgagactgg cagggacgag gacaaatat gatgaggttg agagtgggaa 1080
gcaggagccc agccagctgc gcctgcgctg caggaggcg ggggctctgg ttgtaaaaca 1140
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cacc 1204

<210> 97
<211> 260
<212> PRT
<213> Homo sapiens

<400> 97
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Gly Leu Ser Ala Thr Pro Ala Pro Lys Ser Cys Pro Glu Arg His Tyr
20 25 30
Trp Ala Gln Gly Lys Leu Cys Cys Gln Met Cys Glu Pro Gly Thr Phe
35 40 45
Leu Val Lys Asp Cys Asp Gln His Arg Lys Ala Ala Gln Cys Asp Pro
50 55 60
Cys Ile Pro Gly Val Ser Phe Ser Pro Asp His His Thr Arg Pro His
65 70 75 80
Cys Glu Ser Cys Arg His Cys Asn Ser Gly Leu Leu Val Arg Asn Cys
85 90 95
Thr Ile Thr Ala Asn Ala Glu Cys Ala Cys Arg Asn Gly Trp Gln Cys
100 105 110
Arg Asp Lys Glu Cys Thr Glu Cys Asp Pro Leu Pro Asn Pro Ser Leu
115 120 125
Thr Ala Arg Ser Ser Gln Ala Leu Ser Pro His Pro Gln Pro Thr His
130 135 140
Leu Pro Tyr Val Ser Glu Met Leu Glu Ala Arg Thr Ala Gly His Met
145 150 155 160
Gln Thr Leu Ala Asp Phe Arg Gln Leu Pro Ala Arg Thr Leu Ser Thr
165 170 175
His Trp Pro Pro Gln Arg Ser Leu Cys Ser Ser Asp Phe Ile Arg Ile
180 185 190
Leu Val Ile Phe Ser Gly Met Phe Leu Val Phe Thr Leu Ala Gly Ala
195 200 205
Leu Phe Leu His Gln Arg Arg Lys Tyr Arg Ser Asn Lys Gly Glu Ser
210 215 220
Pro Val Glu Pro Ala Glu Pro Cys Arg Tyr Ser Cys Pro Arg Glu Glu
225 230 235 240
Glu Gly Ser Thr Ile Pro Ile Gln Glu Asp Tyr Arg Lys Pro Glu Pro
245 250 255
Ala Cys Ser Pro
260

<210> 98
<211> 1514
<212> DNA
<213> Homo sapiens

<400> 98
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ctcaacttat tcccttcaat tcaagtaaca ggaaacaaga ttttggtgaa gcagtcgccc 180
atgctttag cgtacgacaa tgcggtcaac cttagctgca agtattccta caatctcttc 240
tcaaggagat tccgggcatc ccttcacaaa ggactggata gtgctgtgga agtctgtgtt 300
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gatatttact tctgcaaaat tgaagtattg tatectctc cttacctaga caatgagaag 480
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ggacatttcta agcccttttg ggtgctgggtg gtggttggtg gagtcctggc ttgctatagc 600
ttgctagtaa cagtggcctt tattatttct tgggtgagga gtaagaggag caggctcctg 660
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WO 2005/037989

PCT/US2003/024918

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ggttaaacgg ggtaagttag agtaggggga gggataggaa gacatatatta aaaaccatta 1260
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<210> 99
<211> 220
<212> PRT
<213> Homo sapiens

<400> 99
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Thr Gly Asn Lys Ile Leu Val Lys Gln Ser Pro Met Leu Val Ala Tyr
20 25 30
Asp Asn Ala Val Asn Leu Ser Cys Lys Tyr Ser Tyr Asn Leu Phe Ser
35 40 45
Arg Glu Phe Arg Ala Ser Leu His Lys Gly Leu Asp Ser Ala Val Glu
50 55 60
Val Cys Val Val Tyr Gly Asn Tyr Ser Gln Gln Leu Gln Val Tyr Ser
65 70 75 80
Lys Thr Gly Phe Asn Cys Asp Gly Lys Leu Gly Asn Glu Ser Val Thr
85 90 95
Phe Tyr Leu Gln Asn Leu Tyr Val Asn Gln Thr Asp Ile Tyr Phe Cys
100 105 110
Lys Ile Glu Val Met Tyr Pro Pro Tyr Leu Asp Asn Glu Lys Ser
115 120 125
Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro
130 135 140
Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly
145 150 155 160
Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile
165 170 175
Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met
180 185 190
Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro
195 200 205
Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser
210 215 220

<210> 100
<211> 672
<212> DNA
<213> Homo sapiens

<400> 100
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ccctgcactc tcctgttttt tcttctcttc atccctgtct tctgcaaagc aatgcacgtg 120
gcccagcctg ctgtgttact ggccagcagc cgaggcatcg ccagctttgt gtgtgagtat 180
gcatctccag gcaaagccac tgaggtccgg gtgacagtgc ttcggcaggc tgacagccag 240
gtgactgaag tctgtgcggc aacctacatg acggggaatg agttgacctt cctagatgat 300
tccatctgca cgggcacctc cagtggaaat caagtgaacc tcactatcca aggactgagg 360
gccatggaca cgggactcta catctgcaag gtggagctca tgtaccacc gccatactac 420
ctgggcatag gcaacggaac ccagatttat gtaattgatc cagaaccgtg ccagatttct 480
gacttcctcc tctggatcct tgcagcagtt agttcggggt tgttttttta tagctttctc 540
ctcacagctg tttcttttag caaaatgcta aagaaaagaa gccctcttac aacaggggtc 600
tatgtgaaaa tgccccaac agagccagaa tgtgaaaagc aatttcagcc ttattttatt 660
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WO 2005/037989

PCT/US2003/024918

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<210> 101
<211> 223
<212> PRT
<213> Homo sapiens

<400> 101
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20 25 30
Val Phe Cys Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala
35 40 45
Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly
50 55 60
Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln
65 70 75 80
Val Thr Glu Val Cys Ala Ala Thr Tyr Met Thr Gly Asn Glu Leu Thr
85 90 95
Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val
100 105 110
Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile
115 120 125
Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly
130 135 140
Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser
145 150 155 160
Asp Phe Leu Leu Trp Ile Leu Ala Ala Val Ser Ser Gly Leu Phe Phe
165 170 175
Tyr Ser Phe Leu Leu Thr Ala Val Ser Leu Ser Lys Met Leu Lys Lys
180 185 190
Arg Ser Pro Leu Thr Thr Gly Val Tyr Val Lys Met Pro Pro Thr Glu
195 200 205
Pro Glu Cys Glu Lys Gln Phe Gln Pro Tyr Phe Ile Pro Ile Asn
210 215 220

<210> 102
<211> 2339
<212> DNA
<213> Homo sapiens

<400> 102
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gacctaggat cagaaacctg gctcctggct cctgctccct actcttctaa ggatcgctgt 180
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ctggctcttc agatctattg tcggaatgaa agcagaggtt gtgcagagca gttaatgctg 600
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gactgcaaag aaaaggctctt gaggaagac ctgagagacc acgtggagaa ggctgtgtaa 720
taccgggaag ccacatgcag ccactgcaag cagatggttc cgatgactgc gctgcgcaaa 780
cacgaagaca ccgactgtcc ctgctgtgtg gtgtcctgcc ctcaacaagt cagcgtccag 840
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ctgagtgtgc acgacatccg cctagccgac atggacctgg gcttccaggt cctggagacc 1440
gccagctaca atggagtgtc catctggaag attcgcgact acaagcggcg gaagcaggag 1500
gccgtcatgg ggaagaccct gtccctttac agccagcctt tctacactgg ttactttggc 1560

WO 2005/037989

PCT/US2003/024918

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 gatacaattt ttattaaagt catagtggat acttcggatc tgcccgatcc ctgataagta 1920
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<210> 103
 <211> 567
 <212> PRT
 <213> Homo sapiens

<400> 103
 Met Glu Ser Ser Lys Lys Met Asp Ser Pro Gly Ala Leu Gln Thr Asn
 1 5 10 15
 Pro Pro Leu Lys Leu His Thr Asp Arg Ser Ala Gly Thr Pro Val Phe
 20 25 30
 Val Pro Glu Gln Gly Gly Tyr Lys Glu Lys Phe Val Lys Thr Val Glu
 35 40 45
 Asp Lys Tyr Lys Cys Glu Lys Cys His Leu Val Leu Cys Ser Pro Lys
 50 55 60
 Gln Thr Glu Cys Gly His Arg Phe Cys Glu Ser Cys Met Ala Ala Leu
 65 70 75 80
 Leu Ser Ser Ser Ser Pro Lys Cys Thr Ala Cys Gln Glu Ser Ile Val
 85 90 95
 Lys Asp Lys Val Phe Lys Asp Asn Cys Cys Lys Arg Glu Ile Leu Ala
 100 105 110
 Leu Gln Ile Tyr Cys Arg Asn Glu Ser Arg Gly Cys Ala Glu Gln Leu
 115 120 125
 Met Leu Gly His Leu Val His Leu Lys Asn Asp Cys His Phe Glu Glu
 130 135 140
 Leu Pro Cys Val Arg Pro Asp Cys Lys Glu Lys Val Leu Arg Lys Asp
 145 150 155 160
 Leu Arg Asp His Val Glu Lys Ala Cys Lys Tyr Arg Glu Ala Thr Cys
 165 170 175
 Ser His Cys Lys Ser Gln Val Pro Met Ile Ala Leu Gln Lys His Glu
 180 185 190
 Asp Thr Asp Cys Pro Cys Val Val Val Ser Cys Pro His Lys Cys Ser
 195 200 205
 Val Gln Thr Leu Leu Arg Ser Glu Leu Ser Ala His Leu Ser Glu Cys
 210 215 220
 Val Asn Ala Pro Ser Thr Cys Ser Phe Lys Arg Tyr Gly Cys Val Phe
 225 230 235 240
 Gln Gly Thr Asn Gln Ile Lys Ala His Glu Ala Ser Ser Ala Val
 245 250 255
 Gln His Val Asn Leu Leu Lys Glu Trp Ser Asn Ser Leu Glu Lys Lys
 260 265 270
 Val Ser Leu Leu Gln Asn Glu Ser Val Glu Lys Asn Lys Ser Ile Gln
 275 280 285
 Ser Leu His Asn Gln Ile Cys Ser Phe Glu Ile Glu Ile Glu Arg Gln
 290 295 300
 Lys Glu Met Leu Arg Asn Asn Glu Ser Lys Ile Leu His Leu Gln Arg
 305 310 315 320
 Val Ile Asp Ser Gln Ala Glu Lys Leu Lys Glu Leu Asp Lys Glu Ile
 325 330 335
 Arg Pro Phe Arg Gln Asn Trp Glu Glu Ala Asp Ser Met Lys Ser Ser
 340 345 350
 Val Glu Ser Leu Gln Asn Arg Val Thr Glu Leu Glu Ser Val Asp Lys
 355 360 365
 Ser Ala Gly Gln Val Ala Arg Asn Thr Gly Leu Leu Glu Ser Gln Leu
 370 375 380
 Ser Arg His Asp Gln Met Leu Ser Val His Asp Ile Arg Leu Ala Asp

WO 2005/037989

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 385 390 395 400
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 405 410 415
 Leu Ile Trp Lys Ile Arg Asp Tyr Lys Arg Arg Lys Gln Glu Ala Val
 420 425 430
 Met Gly Lys Thr Leu Ser Leu Tyr Ser Gln Pro Phe Tyr Thr Gly Tyr
 435 440 445
 Phe Gly Tyr Lys Met Cys Ala Arg Val Tyr Leu Asn Gly Asp Gly Met
 450 455 460
 Gly Lys Gly Thr His Leu Ser Leu Phe Phe Val Ile Met Arg Gly Glu
 465 470 475 480
 Tyr Asp Ala Leu Leu Pro Trp Pro Phe Lys Gln Lys Val Thr Leu Met
 485 490 495
 Leu Met Asp Gln Gly Ser Ser Arg Arg His Leu Gly Asp Ala Phe Lys
 500 505 510
 Pro Asp Pro Asn Ser Ser Ser Phe Lys Lys Pro Thr Gly Glu Met Asn
 515 520 525
 Ile Ala Ser Gly Cys Pro Val Phe Val Ala Gln Thr Val Leu Glu Asn
 530 535 540
 Gly Thr Tyr Ile Lys Asp Asp Thr Ile Phe Ile Lys Val Ile Val Asp
 545 550 555 560
 Thr Ser Asp Leu Pro Asp Pro
 565

<210> 104
 <211> 1874
 <212> DNA
 <213> Homo sapiens

<400> 104
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 caggaatcac aatcccacga aatccaggat gcccaaattc tgaggacaag aacttcccc 180
 ggactgtgat ggtcaacctg aacatccata accggaatac caataccaat cccaaaagg 240
 cctcagatta ctacaaccga tccacctcac ctgggaatct ccaccgcaat gaggaccctg 300
 agagatatcc ctctgtgatc tgggaggcaa agtgccgcca cttgggctgc atcaacgctg 360
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 ctcccccagg cagttagact atggagagcc gaccagagcc ctcaggaacc ctcatccttc 600
 aaagacagcc tcatttcgga ctaaactcat tagagttctt aaggcagttt gtccaattaa 660
 agcttcagag gtaacacttg gccaaagatat gagatctgaa ttacctttcc ctctttccaa 720
 gaaggaagg ttagctgagt accaatttgc ttcttgttta cttttttaag ggctttaagt 780
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 ttacctactt tattttgttt gtctttttta agaagataag attctgggct tgggaatttt 900
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 gtatttagaa aaaggtgaaa aagcactatt atcagttctg cctaggtaaa tgtaagatag 1020
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 tctttgtttt taaaagttat aacatggctg aaaagaaaga ttaaacctac ttcatatgt 1140
 attaatttta attttgcaat ttgttgaggt tttacaagag atacagcaag tctaactctc 1200
 tgttccatta aacccttata ataaaatcct tctgtaataa taaagtttca aaagaaaatg 1260
 tttatttgtt ctcatataat gtatttttagc aaactcagct cttccctatt gggaagagtt 1320
 atgcaaattc tcctataagc aaaacaaagc atgtctttga gtaacaatga cctggaaata 1380
 cccaaaattc caagttctcg atttcacatg ctttcaagac tgaacaccga ctaaggtttt 1440
 catactatta gccaatgctg tagacagaag cttttgata ggaatagagc aaataagata 1500
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 caaaatacaa gaagttctgg gaggagacat tgtcttcaga ctacaatgtc cagtttctcc 1620
 cctagactca ggcttccttt ggagattaag gcccctcaga gatcaacaga ccaacatttt 1680
 tctcttcttc aagcaacact cctagggcct ggttctgtc tgatcaaggc accacacaac 1740
 ccagaaagga gctgatgggg cagaatgaac ttttaagtatg agaaaagttc agcccaagta 1800
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<210> 105
 <211> 155
 <212> PRT
 <213> Homo sapiens

WO 2005/037989

PCT/US2003/024918

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<400> 105
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1 5 10 15
Leu Glu Ala Ile Val Lys Ala Gly Ile Thr Ile Pro Arg Asn Pro Gly
20 25 30
Cys Pro Asn Ser Glu Asp Lys Asn Phe Pro Arg Thr Val Met Val Asn
35 40 45
Leu Asn Ile His Asn Arg Asn Thr Asn Thr Asn Pro Lys Arg Ser Ser
50 55 60
Asp Tyr Tyr Asn Arg Ser Thr Ser Pro Trp Asn Leu His Arg Asn Glu
65 70 75 80
Asp Pro Glu Arg Tyr Pro Ser Val Ile Trp Glu Ala Lys Cys Arg His
85 90 95
Leu Gly Cys Ile Asn Ala Asp Gly Asn Val Asp Tyr His Met Asn Ser
100 105 110
Val Pro Ile Gln Glu Ile Leu Val Leu Arg Arg Glu Pro Pro His
115 120 125
Cys Pro Asn Ser Phe Arg Leu Glu Lys Ile Leu Val Ser Val Gly Cys
130 135 140
Thr Cys Val Thr Pro Ile Val His His Val Ala
145 150 155

<210> 106
<211> 3120
<212> DNA
<213> Homo sapiens

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gcgcctccct gcgactcctg gaccacccgg cgctgggtctg ctcccagccg gggctaaact 180
gcacgggtcaa gaatagtacc tgcttgatg acagctggat tcaccctcga aacctgacct 240
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WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
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 <212> PRT
 <213> Homo sapiens

<400> 107
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 35 40 45
 Asn Cys Thr Val Lys Asn Ser Thr Cys Leu Asp Asp Ser Trp Ile His
 50 55 60
 Pro Arg Asn Leu Thr Pro Ser Ser Pro Lys Asp Leu Gln Ile Gln Leu
 65 70 75 80
 His Phe Ala His Thr Gln Gln Gly Asp Leu Phe Pro Val Ala His Ile
 85 90 95
 Glu Trp Thr Leu Gln Thr Asp Ala Ser Ile Leu Tyr Leu Glu Gly Ala
 100 105 110
 Glu Leu Ser Val Leu Gln Leu Asn Thr Asn Glu Arg Leu Cys Val Arg
 115 120 125
 Phe Glu Phe Leu Ser Lys Leu Arg His His His Arg Arg Trp Arg Phe
 130 135 140
 Thr Phe Ser His Phe Val Val Asp Pro Asp Gln Tyr Glu Val Thr
 145 150 155 160
 Val His His Leu Pro Lys Pro Ile Pro Asp Gly Asp Pro Asn His Gln
 165 170 175
 Ser Lys Asn Phe Leu Val Pro Asp Cys Glu His Ala Arg Met Lys Val
 180 185 190
 Thr Thr Pro Cys Met Ser Ser Gly Ser Leu Trp Asp Pro Asn Ile Thr
 195 200 205
 Val Glu Thr Leu Glu Ala His Gln Leu Arg Val Ser Phe Thr Leu Trp
 210 215 220
 Asn Glu Ser Thr His Tyr Gln Ile Leu Leu Thr Ser Phe Pro His Met
 225 230 235 240
 Glu Asn His Ser Cys Phe Glu His Met His Ile Pro Ala Pro Arg
 245 250 255
 Pro Glu Glu Phe His Gln Arg Ser Asn Val Thr Leu Thr Leu Arg Asn
 260 265 270
 Leu Lys Gly Cys Cys Arg His Gln Val Gln Ile Gln Pro Phe Phe Ser
 275 280 285
 Ser Cys Leu Asn Asp Cys Leu Arg His Ser Ala Thr Val Ser Cys Pro
 290 295 300
 Glu Met Pro Asp Thr Pro Glu Pro Ile Pro Asp Tyr Met Pro Leu Trp
 305 310 315 320
 Val Tyr Trp Phe Ile Thr Gly Ile Ser Ile Leu Leu Val Gly Ser Val
 325 330 335
 Ile Leu Leu Ile Val Cys Met Thr Trp Arg Leu Ala Gly Pro Gly Ser
 340 345 350
 Glu Lys Tyr Ser Asp Asp Thr Lys Tyr Thr Asp Gly Leu Pro Ala Ala
 355 360 365
 Asp Leu Ile Pro Pro Pro Leu Lys Pro Arg Lys Val Trp Ile Ile Tyr
 370 375 380
 Ser Ala Asp His Pro Leu Tyr Val Asp Val Val Leu Lys Phe Ala Gln

WO 2005/037989

PCT/US2003/024918

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 Glu Gln Ala Ile Ser Glu Ala Gly Val Met Thr Trp Val Gly Arg Gln
 420 425 430
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 435 440 445
 Arg Gly Thr Arg Ala Lys Trp Gln Ala Leu Leu Gly Arg Gly Ala Pro
 450 455 460
 Val Arg Leu Arg Cys Asp His Gly Lys Pro Val Gly Asp Leu Phe Thr
 465 470 475 480
 Ala Ala Met Asn Met Ile Leu Pro Asp Phe Lys Arg Pro Ala Cys Phe
 485 490 495
 Gly Thr Tyr Val Val Cys Tyr Phe Ser Glu Val Ser Cys Asp Gly Asp
 500 505 510
 Val Pro Asp Leu Phe Gly Ala Ala Pro Arg Tyr Pro Leu Met Asp Arg
 515 520 525
 Phe Glu Glu Val Tyr Phe Arg Ile Gln Asp Leu Glu Met Phe Gln Pro
 530 535 540
 Gly Arg Met His Arg Val Gly Glu Leu Ser Gly Asp Asn Tyr Leu Arg
 545 550 555 560
 Ser Pro Gly Gly Arg Gln Leu Arg Ala Ala Leu Asp Arg Phe Arg Asp
 565 570 575
 Trp Gln Val Arg Cys Pro Asp Trp Phe Glu Cys Glu Asn Leu Tyr Ser
 580 585 590
 Ala Asp Asp Gln Asp Ala Pro Ser Leu Asp Glu Glu Val Phe Glu Glu
 595 600 605
 Pro Leu Leu Pro Pro Gly Thr Ile Val Lys Arg Ala Pro Leu Val
 610 615 620
 Arg Glu Pro Gly Ser Gln Ala Cys Leu Ala Ile Asp Pro Leu Val Gly
 625 630 635 640
 Glu Glu Gly Gly Ala Val Ala Lys Leu Glu Pro His Leu Gln Pro
 645 650 655
 Arg Gly Gln Pro Ala Pro Gln Pro Leu His Thr Leu Val Leu Ala Ala
 660 665 670
 Glu Glu Gly Ala Leu Val Ala Ala Val Glu Pro Gly Pro Ala Asp
 675 680 685
 Gly Ala Ala Val Arg Leu Ala Leu Ala Gly Glu Gly Glu Ala Cys Pro
 690 695 700
 Leu Leu Gly Ser Pro Gly Ala Gly Arg Asn Ser Val Leu Phe Leu Pro
 705 710 715 720
 Val Asp Pro Glu Asp Ser Pro Leu Gly Ser Ser Thr Pro Met Ala Ser
 725 730 735 740
 Pro Asp Leu Leu Pro Glu Asp Val Arg Glu His Leu Glu Gly Leu Met
 745 750 755
 Leu Ser Leu Phe Glu Gln Ser Leu Ser Cys Gln Ala Gln Gly Gly Cys
 760 765 770
 Ser Arg Pro Ala Met Val Leu Thr Asp Pro His Thr Pro Tyr Glu Glu
 775 780 785
 Glu Gln Arg Gln Ser Val Gln Ser Asp Gln Gly Tyr Ile Ser Arg Ser
 790 795 800
 Ser Pro Gln Pro Pro Gly Leu Thr Glu Met Glu Glu Glu Glu Glu
 805 810 815
 Glu Glu Gln Asp Pro Gly Lys Pro Ala Leu Pro Leu Ser Pro Glu Asp
 820 825 830
 Leu Glu Ser Leu Arg Ser Leu Gln Arg Gln Leu Leu Phe Arg Gln Leu
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 Ser Ala
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WO 2005/037989

PCT/US2003/024918

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 <212> PRT
 <213> Homo sapiens

<400> 109
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 35 40 45
 Asp Ala Cys Leu Ile Thr Lys Ala Gly Leu Gln Val Tyr Asn Lys Cys
 50 55 60
 Trp Lys Phe Glu His Cys Asn Phe Asn Asp Val Thr Thr Arg Leu Arg
 65 70 75 80
 Glu Asn Glu Leu Thr Tyr Tyr Cys Cys Lys Lys Asp Leu Cys Asn Phe
 85 90 95
 Asn Glu Gln Leu Glu Asn Gly Gly Thr Ser Leu Ser Glu Lys Thr Val
 100 105 110
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 115 120 125

<210> 110
 <211> 1048
 <212> DNA
 <213> Homo sapiens

<400> 110
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 agtactttga atccaaatct aaaggcaggg tcagacttga tcctcagagt ggcgcactgt 300
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 taaaaagata taattataaa aaaaaaaa 1048

<210> 111
 <211> 243
 <212> PRT
 <213> Homo sapiens

<400> 111
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WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

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| Met | Thr | Val | Val | Ser | Gly | Ser | Asn | Val | Thr | Leu | Asn | Ile | Ser | Glu | Ser |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Leu | Pro | Glu | Asn | Tyr | Lys | Gln | Leu | Thr | Trp | Phe | Tyr | Thr | Phe | Asp | Gln |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Lys | Ile | Val | Glu | Trp | Asp | Ser | Arg | Lys | Ser | Lys | Tyr | Phe | Glu | Ser | Lys |
| 65 | | | | | 70 | | | | | 75 | | | | 80 | |
| Phe | Lys | Gly | Arg | Val | Arg | Leu | Asp | Pro | Gln | Ser | Gly | Ala | Leu | Tyr | Ile |
| | | | 85 | | | | | 90 | | | | | 95 | | |
| Ser | Lys | Val | Gln | Lys | Glu | Asp | Asn | Ser | Thr | Tyr | Ile | Met | Arg | Val | Leu |
| | | 100 | | | | | | 105 | | | | 110 | | | |
| Lys | Lys | Thr | Gly | Asn | Glu | Gln | Glu | Trp | Lys | Ile | Lys | Leu | Gln | Val | Leu |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Asp | Pro | Val | Pro | Lys | Pro | Val | Ile | Lys | Ile | Glu | Lys | Ile | Glu | Asp | Met |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Asp | Asp | Asn | Cys | Tyr | Leu | Lys | Leu | Ser | Cys | Val | Ile | Pro | Gly | Glu | Ser |
| 145 | | | | | 150 | | | | | 155 | | | | 160 | |
| Val | Asn | Tyr | Thr | Trp | Tyr | Gly | Asp | Lys | Arg | Pro | Phe | Pro | Lys | Glu | Leu |
| | | | 165 | | | | | 170 | | | | | | 175 | |
| Gln | Asn | Ser | Val | Leu | Glu | Thr | Thr | Leu | Met | Pro | His | Asn | Tyr | Ser | Arg |
| | | 180 | | | | | | 185 | | | | | 190 | | |
| Cys | Tyr | Thr | Cys | Gln | Val | Ser | Asn | Ser | Val | Ser | Ser | Lys | Asn | Gly | Thr |
| | 195 | | | | | | 200 | | | | | 205 | | | |
| Val | Cys | Leu | Ser | Pro | Pro | Cys | Thr | Leu | Ala | Arg | Ser | Phe | Gly | Val | Glu |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Trp | Ile | Ala | Ser | Trp | Leu | Val | Val | Thr | Val | Pro | Thr | Ile | Leu | Gly | Leu |
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| Leu | Leu | Thr | | | | | | | | | | | | | |

<210> 112
<211> 1040
<212> DNA
<213> Homo sapiens

<400> 112

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| tgcctgctgc | actgctttgg | tttcatcagc | tgtttttccc | aacaaatata | tggtgtttgtg | 120 |
| tatgggaatg | taactttcca | tgtaccaagc | aatgtgcctt | taaaagaggt | cctatggaaa | 180 |
| aaacaaaagg | ataaagttgc | agaactggaa | aattctgaat | tcagagcttt | ctcatctttt | 240 |
| aaaaataggg | tttatttaga | cactgtgtca | ggtagcctca | ctatctacaa | cttaacatca | 300 |
| tcagatgaag | atgagtatga | aatggaatcg | ccaaatatta | ctgataccat | gaagttcttt | 360 |
| ctttatgtgc | ttgagtctct | tccatctccc | acactaactt | gtgcattgac | taatggaagc | 420 |
| attgaagtcc | aatgcatgat | accagagcat | tacaacagcc | atcgaggact | tataatgtac | 480 |
| tcatgggatt | gtcctatgga | gcaatgtaaa | cgtaactcaa | ccagtatata | ttttaagatg | 540 |
| gaaaatgatk | ttccacaaaa | aatacagtgt | actcttagca | atccattatt | taataaca | 600 |
| tcatcaatca | ttttgacaac | ctgtatccca | agcagcggtc | attcaagaca | cagatatgca | 660 |
| cttataccca | taccattagc | agtaattaca | acatgtattg | tgctgtatat | gaatgggtatt | 720 |
| ctgaaatgtg | acagaaaacc | agacagaacc | aactccaatt | gattggtaac | agaagatgaa | 780 |
| gacaacagca | taactaaatt | attttaaaaa | ctaaaaagcc | atctgatttc | tcatttgagt | 840 |
| attacaattt | ttgaacaact | gttggaatg | taacttgaag | cagctgcttt | aagaagaaat | 900 |
| accactaac | aaagaacaag | cattagtttt | ggctgtcatc | aacttattat | atgactaggt | 960 |
| gcttgctttt | ttgtcagta | aattgttttt | actgatgatg | tagatacttt | tgtaaataaa | 1020 |
| tgtaaataatg | tacacaagtg | | | | | 1040 |

<210> 113
<211> 250
<212> PRT
<213> Homo sapiens

<400> 113

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| Met | Val | Ala | Gly | Ser | Asp | Ala | Gly | Arg | Ala | Leu | Gly | Val | Leu | Ser | Val |
| 1 | | | | 5 | | | | 10 | | | | | 15 | | |
| Val | Cys | Leu | Leu | His | Cys | Phe | Gly | Phe | Ile | Ser | Cys | Phe | Ser | Gln | Gln |
| | | 20 | | | | | | 25 | | | | 30 | | | |
| Ile | Tyr | Gly | Val | Val | Tyr | Gly | Asn | Val | Thr | Phe | His | Val | Pro | Ser | Asn |
| | 35 | | | | | 40 | | | | | 45 | | | | |
| Val | Pro | Leu | Lys | Glu | Val | Leu | Trp | Lys | Lys | Gln | Lys | Asp | Lys | Val | Ala |

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

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| 50 | 55 | 60 |
| Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe Lys Asn Arg | | |
| 65 Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr Asn Leu Thr | 70 | 80 |
| | 85 | 90 |
| Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn Ile Thr Asp | 100 | 110 |
| Thr Met Lys Phe Phe Leu Tyr Val Leu Glu Ser Leu Pro Ser Pro Thr | 115 | 120 |
| Leu Thr Cys Ala Leu Thr Asn Gly Ser Ile Glu Val Gln Cys Met Ile | 130 | 140 |
| Pro Glu His Tyr Asn Ser His Arg Gly Leu Ile Met Tyr Ser Trp Asp | 145 | 155 |
| Cys Pro Met Glu Gln Cys Lys Arg Asn Ser Thr Ser Ile Tyr Phe Lys | 165 | 175 |
| Met Glu Asn Asp Leu Pro Gln Lys Ile Gln Cys Thr Leu Ser Asn Pro | 180 | 190 |
| Leu Phe Asn Thr Thr Ser Ser Ile Ile Leu Thr Thr Cys Ile Pro Ser | 195 | 205 |
| Ser Gly His Ser Arg His Arg Tyr Ala Leu Ile Pro Ile Pro Leu Ala | 210 | 220 |
| Val Ile Thr Thr Cys Ile Val Leu Tyr Met Asn Gly Ile Leu Lys Cys | 225 | 235 |
| Asp Arg Lys Pro Asp Arg Thr Asn Ser Asn | 245 | 250 |

<210> 114
<211> 1358
<212> DNA
<213> Homo sapiens

<400> 114

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| tgcgctttgt | gaaagtgtccc | ctgaagaaca | gcgcattctaa | ccatctagga | caggactgtg | 120 |
| aggcctatga | agatggggaa | ctcacctacg | agaacgtgca | agtgtctcca | gtcccaggag | 180 |
| ggccaccagg | cttggcttcc | cctgcactag | cggacaaagc | aggggtcggg | tcagagcaac | 240 |
| caactgcgac | ctggagctct | gtgaagtcgt | ctgctctcag | gcagattccc | cgctgtccta | 300 |
| cggtctgtct | gcaaaacttc | ttgcttggcc | ttctctctgc | ctgtctgatg | ttaggggttg | 360 |
| ctgtcatctg | cctgggagtt | cgctatctgc | agggtgtctca | gcagttccag | gaggggacca | 420 |
| ggatttggga | agccaccaat | agcagcctgc | agcagcagct | cagggagaag | ataagtcagc | 480 |
| tggggcagaa | ggaggttgag | cttcaggagt | ctcagaaaga | gctgatctcg | agccaggaca | 540 |
| cattacagga | gaagcagagg | actcacaagg | acactgagca | gcaactacaa | gcctgtccagg | 600 |
| ctgagagagc | gaagaccaag | gagaacctga | aaactgagga | ggagcggagg | agggacctgg | 660 |
| accagagggt | gacaagcacg | cgggagacac | tgaggcgctt | gtcctcctgt | tcacagacac | 720 |
| cctgtgttcc | atgctggatg | attccatatc | aggaaagggt | cttttacatc | tcacataccc | 780 |
| tcagaagtct | ggaggagagc | caaaaatact | gcacatctct | gtcctccaaa | ctggcagcat | 840 |
| tcgatgaacc | ttctaagtat | tactatgaat | acctctctga | cgccccccag | gtttctctgc | 900 |
| ccagcggctt | agaggagtgt | ctagatcggt | cgaagtcata | ttggatacag | atgagcaaga | 960 |
| agtggaggca | tgactatgac | tctcaaagcc | gatattgtga | caagataaaa | aaatattacc | 1020 |
| agaagtggaa | aagaacattt | tctgagtgtg | cagagcttca | cccctgcatt | tgtgagtcgg | 1080 |
| aggctttcag | gtttcctgat | gggatccatc | tgaactgaac | cgataacttg | aacaagacct | 1140 |
| tgtgacctac | atccttaacc | taaggcctgc | caatttttaa | gactgctatt | cctccagcac | 1200 |
| tcctcactc | tcgggcatgc | ccagctaagg | gatgacctgc | tgcttgcttg | aaagctgctc | 1260 |
| cagaaactgg | actactcttg | ggaagagtaa | agaagcctcc | agaaaagact | tgaccttcct | 1320 |
| taaatacttc | ccaaactaga | gatgggtcag | gggagggc | | | 1358 |

<210> 115
<211> 359
<212> PRT
<213> Homo sapiens

<400> 115

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| Met Ala Asp Ala Ile Thr Tyr Ala Asp Leu Arg Phe Val Lys Val Pro | 1 | 5 | 10 | 15 |
| Leu Lys Asn Ser Ala Ser Asn His Leu Gly Gln Asp Cys Glu Ala Tyr | 20 | 25 | 30 | |
| Glu Asp Gly Glu Leu Thr Tyr Glu Asn Val Gln Val Ser Pro Val Pro | 35 | 40 | 45 | |

PCT/US2003/024918

<210> 117
<211> 195
<212> PRT
<213> Mus musculus

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
<400> 117
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Ala Phe Gln Arg Gln Trp Pro Trp Leu Leu Val Val Phe Ile Thr
20 25 30
Val Phe Cys Cys Trp Phe His Cys Ser Gly Leu Leu Ser Lys Gln Gln
35 40 45
Gln Arg Leu Leu Glu His Pro Glu Pro His Thr Ala Glu Leu Gln Leu
50 55 60
Asn Leu Thr Val Pro Arg Lys Asp Pro Thr Leu Arg Trp Gly Ala Gly
65 70 75 80
Pro Ala Leu Gly Arg Ser Phe Thr His Gly Pro Glu Leu Glu Gly
85 90 95
His Leu Arg Ile His Gln Asp Gly Leu Tyr Arg Leu His Ile Gln Val
100 105 110
Thr Leu Ala Asn Cys Ser Ser Pro Gly Ser Thr Leu Gln His Arg Ala
115 120 125
Thr Leu Ala Val Gly Ile Cys Ser Pro Ala Ala His Gly Ile Ser Leu
130 135 140
Leu Arg Gly Arg Phe Gly Gln Asp Cys Thr Val Ala Leu Gln Arg Leu
145 150 155 160
Thr Tyr Leu Val His Gly Asp Val Leu Cys Thr Asn Leu Thr Leu Pro
165 170 175
Leu Leu Pro Ser Arg Asn Ala Asp Glu Thr Phe Phe Gly Val Gln Trp
180 185 190
Ile Cys Pro
195

<210> 118
<211> 909
<212> DNA
<213> Homo sapiens

<400> 118
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gaaggaaagg gttttgattt aaatgatgtt tacgtatatt ggcaaaccag tgagtcgaaa 180
accgtgggtga cctaccacat cccacagaac agctccttgg aaaacgtgga cagccgctac 240
cggaaccgag ccctgatgtc accggccggc atgctgcggg gcgacttctc cctgcgcttg 300
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cttctgcagc agaactgac tgtcggcagc cagacaggaa atgacatcgg agagagagac 720
aagatcacag agaatccagt cagtaccggc gagaaaaacg cggccacgtg gagcatcctg 780
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cacgtttga 909

<210> 119
<211> 302
<212> PRT
<213> Homo sapiens

<400> 119
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1 5 10 15
Arg Ala Asp Thr Gln Glu Lys Glu Val Arg Ala Met Val Gly Ser Asp
20 25 30
Val Glu Leu Ser Cys Ala Cys Pro Glu Gly Ser Arg Phe Asp Leu Asn
35 40 45
Asp Val Tyr Val Tyr Trp Gln Thr Ser Glu Ser Lys Thr Val Val Thr
50 55 60
Tyr His Ile Pro Gln Asn Ser Ser Leu Glu Asn Val Asp Ser Arg Tyr
65 70 75 80
Arg Asn Arg Ala Leu Met Ser Pro Ala Gly Met Leu Arg Gly Asp Phe

PCT/US2003/024918

<400> 121
Met Gly Leu Ser Asn Ile Leu Phe Val Met Ala Phe Leu Leu Ser Gly
1 5 10 15
Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr Ala Asp Leu

PCT/US2003/024918

| | | | | | | | |
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| acttctcccc | gatctgcggc | cactggactg | cccacagca | tgaaaatfff | tatgtattta | 120 | |
| cttactgttt | ttcttatcac | ccagatgatt | gggtcagcac | tttttgcgtg | gtatcttcat | 180 | |
| agaaggttgg | acaagataga | agatgaaagg | aaatcttcag | aagattttgg | attcatgaaa | 240 | |
| acgatacaga | gatgcaacac | aggagaaaga | tccttatcct | tactgaactg | tgaggagatt | 300 | |
| aaaagccagt | ttgaaggcct | tgtgaaggat | ataatgttaa | acaagaagga | gacgaagaaa | 360 | |
| gaaaacagct | ttgaaatgca | aaaaggtgat | cagaatctct | aaattgcggc | acatgtcata | 420 | |
| agtgaggcca | gcagtaaaac | aacatctgtg | ttacagtggg | ctgaaaaagg | atactacacc | 480 | |
| atgagcaaca | acttggtaac | cctggaaaaa | gggaaacagc | tgaccgttaa | aagacaagga | 540 | |
| ctctattata | ttctatgccca | agtcaccttc | tgttccaatc | gggaagcttc | gagtcaagct | 600 | |
| ccatttatag | ccagcctctg | cttaaagtc | ccgggtagat | tcgagagaat | cttactcaga | 660 | |
| gctgcaaata | cccacagttc | cgccaaacct | tgcgggcaac | aatccattca | cttgggagga | 720 | |
| gtatttgaat | tgcaaccagg | tgcttctggt | tttgtcaatg | tgactgatcc | aagccaagtg | 780 | |
| agccattggca | ctggcttcac | gtccttttgc | ttactcaaac | ttctgaacatg | gtcaccttgc | 840 | |
| aggctgtggg | ggagctgacg | ctgggagctc | tcataataca | gcacagcggg | taagcccacc | 900 | |
| ccctgttaac | tgccatttta | taaccctagg | atcctcctta | tggagaacta | tttattatac | 960 | |
| actccaaggc | atgtagaact | gtaataagtg | aattacaggt | cacatgaaac | caaaacgggc | 1020 | |
| ccctgtccat | aaagacttat | atatctgaag | cagcaacccc | actgatgcag | acatccagag | 1080 | |
| agtcctatga | aaagacaagg | ccattatgca | caggttgaat | cttgagtaaa | cagcagataa | 1140 | |
| cttgccaagt | tcagttttgt | ttctttgcgt | gcagtgctct | tccatggata | atgcatttga | 1200 | |
| tttatcagtg | aagatgcaga | agggaaatgg | ggagcctcag | ctcacattca | gttatggttg | 1260 | |
| actctggggt | ccctatggct | tgtttggagg | ggccaggctc | tagaacctct | aacacagatg | 1320 | |
| agaaccgaaa | ccccccccc | cccccccgcc | accctctcgg | acagttattc | atttctcttc | 1380 | |

WO 2005/037989

PCT/US2003/024918

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<210> 123
<211> 261
<212> PRT
<213> Homo sapiens

<400> 123
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20 25 30
Ile Thr Gln Met Ile Gly Ser Ala Leu Phe Ala Val Tyr Leu His Arg
35 40 45
Arg Leu Asp Lys Ile Glu Asp Gln Arg Asn Leu His Glu Asp Phe Val
50 55 60
Phe Met Lys Thr Ile Gln Arg Cys Asn Thr Gly Glu Arg Ser Leu Ser
65 70 75 80
Leu Leu Asn Cys Glu Ile Lys Ser Gln Phe Glu Gly Phe Val Lys
85 90 95
Asp Ile Met Leu Asn Lys Glu Glu Thr Lys Lys Glu Asn Ser Phe Glu
100 105 110
Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala His Val Ile Ser
115 120 125
Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp Ala Glu Lys Gly
130 135 140
Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu Glu Asn Gly Lys Gln
145 150 155 160
Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr
165 170 175
Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser
180 185 190
Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu Arg Ala
195 200 205
Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser Ile His
210 215 220
Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser Val Phe Val Asn
225 230 235 240
Val Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe
245 250 255
Gly Leu Leu Lys Leu
260

<210> 124
<211> 1879
<212> DNA
<213> Homo sapiens

<400> 124
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cccagctctt gctcctgcct gtttgccctg aaatggccac gcttctcctt ctcttgggg 120
tgctggtggt aagcccagac gctctgggga gcacaacagc agtcgagaca cccacctccg 180
gagagccttt ggtctctact agcagacccc tgagctcaaa gatgtacacc acttcaataa 240
caagtgaccc taaggccgac agcactgggg accagacctc agccctacct cctcaactt 300
ccatcaatga gggatcccct ctttggaact ccattgggtg cagcactggg tcccctttac 360
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caactgactc tctggagacc tccactggga ccactggacc ccctgttacc atgacaactg 720

WO 2005/037989

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<210> 125
<211> 400
<212> PRT
<213> Homo sapiens

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<400> 125
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20     25     30
Leu Val Ser Thr Ser Glu Pro Leu Ser Ser Lys Met Tyr Thr Thr Ser
35     40     45
Ile Thr Ser Asp Pro Lys Ala Asp Ser Thr Gly Asp Gln Thr Ser Ala
50     55     60
Leu Pro Pro Ser Thr Ser Ile Asn Glu Gly Ser Pro Leu Trp Thr Ser
65     70     75     80
Ile Gly Ala Ser Thr Gly Ser Pro Leu Pro Glu Pro Thr Thr Tyr Gln
85     90     95
Glu Val Ser Ile Lys Met Ser Ser Val Pro Gln Glu Thr Pro His Ala
100    105    110
Thr Ser His Pro Ala Val Pro Ile Thr Ala Asn Ser Leu Gly Ser His
115    120    125
Thr Val Thr Gly Gly Thr Ile Thr Thr Asn Ser Pro Glu Thr Ser Ser
130    135    140
Arg Thr Ser Gly Ala Pro Val Thr Thr Ala Ala Ser Ser Leu Glu Thr
145    150    155    160
Ser Arg Gly Thr Ser Gly Pro Pro Leu Thr Met Ala Thr Val Ser Leu
165    170    175
Glu Thr Ser Lys Gly Thr Ser Gly Pro Pro Val Thr Met Ala Thr Asp
180    185    190
Ser Leu Glu Thr Ser Thr Gly Thr Thr Gly Pro Pro Val Thr Met Thr
195    200    205
Thr Gly Ser Leu Glu Pro Ser Ser Gly Ala Ser Gly Pro Gln Val Ser
210    215    220
Ser Val Lys Leu Ser Thr Met Met Ser Pro Thr Thr Ser Thr Asn Ala
225    230    235    240
Ser Thr Val Pro Phe Arg Asn Pro Asp Glu Asn Ser Arg Gly Met Leu
245    250    255
Pro Val Ala Val Leu Val Ala Leu Leu Ala Val Ile Val Leu Val Ala
260    265    270
Leu Leu Leu Leu Trp Arg Arg Arg Gln Lys Arg Arg Thr Gly Ala Leu
275    280    285
Val Leu Ser Arg Gly Gly Lys Arg Asn Gly Val Val Asp Ala Trp Ala
290    295    300
Gly Pro Ala Gln Val Pro Glu Glu Gly Ala Val Thr Val Thr Val Gly
305    310    315    320
Gly Ser Gly Gly Asp Lys Gly Ser Gly Phe Pro Asp Gly Glu Gly Ser
325    330    335

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WO 2005/037989

PCT/US2003/024918

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Gln Gly Ser Leu Ala Met Glu Glu Leu Lys Ser Gly Ser Gly Pro Ser
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Leu Lys Gly Glu Glu Glu Pro Leu Val Ala Ser Glu Asp Gly Ala Val
370 375 380
Asp Ala Pro Ala Pro Asp Glu Pro Glu Gly Gly Asp Gly Ala Ala Pro
385 390 395 400

<210> 126
<211> 3567
<212> DNA
<213> Homo sapiens

<400> 126
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WO 2005/037989

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<210> 127
<211> 1038
<212> PRT
<213> Homo sapiens

<400> 127
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20 25 30
Gly Val Pro Thr Gly Arg Pro Tyr Asn Val Asp Thr Glu Ser Ala Leu
35 40 45
Leu Tyr Gln Gly Pro His Asn Thr Leu Phe Gly Tyr Ser Val Val Leu
50 55 60
His Ser His Gly Ala Asn Arg Trp Leu Leu Val Gly Ala Pro Thr Ala
65 70 75 80
Asn Trp Leu Ala Asn Ala Ser Val Ile Asn Pro Gly Ala Ile Tyr Arg
85 90 95
Cys Arg Ile Gly Lys Asn Pro Gly Gln Thr Cys Glu Gln Leu Gln Leu
100 105 110
Gly Ser Pro Asn Gly Glu Pro Cys Gly Lys Thr Cys Leu Glu Glu Arg
115 120 125
Asp Asn Gln Trp Leu Gly Val Thr Leu Ser Arg Gln Pro Gly Glu Asn
130 135 140
Gly Ser Ile Val Thr Cys Gly His Arg Trp Lys Asn Ile Phe Tyr Ile
145 150 155 160
Lys Asn Glu Asn Lys Leu Pro Thr Gly Gly Cys Tyr Gly Val Pro Pro
165 170 175
Asp Leu Arg Thr Glu Leu Ser Lys Arg Ile Ala Pro Cys Tyr Gln Asp
180 185 190
Tyr Val Lys Lys Phe Gly Glu Asn Phe Ala Ser Cys Gln Ala Gly Ile
195 200 205
Ser Ser Phe Tyr Thr Lys Asp Leu Ile Val Met Gly Ala Pro Gly Ser
210 215 220
Ser Tyr Trp Thr Gly Ser Leu Phe Val Tyr Asn Ile Thr Thr Asn Lys
225 230 235 240
Tyr Lys Ala Phe Leu Asp Lys Gln Asn Gln Val Lys Phe Gly Ser Tyr
245 250 255
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WO 2005/037989

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WO 2005/037989

PCT/US2003/024918

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| Leu | Gly | Gly | Leu | Gly | Cys | Gly | Leu | Lys | Asn | Arg | Ser | Ser | Glu | Gly | Pro |
| | | | 130 | | | 135 | | | | | 140 | | | | |
| Ser | Ser | Pro | Ser | Gly | Lys | Leu | Met | Ser | Pro | Lys | Leu | Tyr | Val | Trp | Ala |
| 145 | | | | | 150 | | | | | 155 | | | | 160 | |
| Lys | Asp | Arg | Pro | Glu | Ile | Trp | Glu | Gly | Glu | Pro | Pro | Cys | Val | Pro | Pro |
| | | | 165 | | | | | 170 | | | | | | 175 | |
| Arg | Asp | Ser | Leu | Asn | Gln | Ser | Leu | Ser | Gln | Asp | Leu | Thr | Met | Ala | Pro |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Gly | Ser | Thr | Leu | Trp | Leu | Ser | Cys | Gly | Val | Pro | Pro | Asp | Ser | Val | Ser |
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| | | | 210 | | | 215 | | | | | 220 | | | | |
| Leu | Leu | Ser | Leu | Glu | Leu | Lys | Asp | Asp | Arg | Pro | Ala | Arg | Asp | Met | Trp |
| 225 | | | | | 230 | | | | | 235 | | | | 240 | |
| Val | Met | Glu | Thr | Gly | Leu | Leu | Leu | Pro | Arg | Ala | Thr | Ala | Gln | Asp | Ala |
| | | | | 245 | | | | 250 | | | | | | 255 | |
| Gly | Lys | Tyr | Tyr | Cys | His | Arg | Gly | Asn | Leu | Thr | Met | Ser | Phe | His | Leu |
| | | | 260 | | | | | 265 | | | | | 270 | | |
| Glu | Ile | Thr | Ala | Arg | Pro | Val | Leu | Trp | His | Trp | Leu | Leu | Arg | Thr | Gly |
| | | | 275 | | | | 280 | | | | | 285 | | | |
| Gly | Trp | Lys | Val | Ser | Ala | Val | Thr | Leu | Ala | Tyr | Leu | Ile | Phe | Cys | Leu |
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WO 2005/037989

PCT/US2003/024918

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 Thr Pro Pro Pro Gly Ser Gly Pro Gln Asn Gln Tyr Gly Asn Val Leu
 340 345 350
 Ser Leu Pro Thr Pro Thr Ser Gly Leu Gly Arg Ala Gln Arg Trp Ala
 355 360 365
 Ala Gly Leu Gly Gly Thr Ala Pro Ser Tyr Gly Asn Pro Ser Ser Asp
 370 375 380
 Val Gln Ala Asp Gly Ala Leu Gly Ser Arg Ser Pro Pro Gly Val Gly
 385 390 395 400
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 Asp Ser Glu Phe Tyr Glu Asn Asp Ser Asn Leu Gly Gln Asp Gln Leu
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 Asp Glu Glu Leu Thr Gln Pro Val Ala Arg Thr Met Asp Phe Leu Ser
 465 470 475 480
 Pro His Gly Ser Ala Trp Asp Pro Ser Arg Glu Ala Thr Ser Leu Gly
 485 490 495
 Ser Gln Ser Tyr Glu Asp Met Arg Gly Ile Leu Tyr Ala Ala Pro Gln
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 Leu Arg Ser Ile Arg Gly Gln Pro Gly Pro Asn His Glu Glu Asp Ala
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WO 2005/037989

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Cys Val Thr Val Trp Tyr Pro Leu Trp Gly Gly Ile Met Tyr Ile Ile
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Ser Gly Ser Leu Leu Ala Ala Thr Glu Lys Asn Ser Arg Lys Cys Leu
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His Phe Leu Lys Met Glu Ser Leu Asn Phe Ile Arg Ala His Thr Pro
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Tyr Ile Asn Ile Tyr Asn Cys Glu Pro Ala Asn Pro Ser Glu Lys Asn
165 170 175
Ser Pro Ser Thr Gln Tyr Cys Tyr Ser Ile Gln Ser Leu Phe Leu Gly
180 185 190
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195 200 205
Ala Gly Ile Val Glu Asn Glu Trp Lys Arg Thr Cys Ser Arg Pro Lys
210 215 220
Ser Asn Ile Val Leu Leu Ser Ala Glu Glu Lys Lys Glu Gln Thr Ile
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Lys Asn Glu Glu Asp Ile Glu Ile Ile Pro Ile Gln Glu Glu Glu
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WO 2005/037989

PCT/US2003/024918

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| gaaactcggg | cagcctccaa | tgtgacttct | caagcagcca | ccccaagaa | gtccagttct | 1680 |
| tctgggagaa | aaatggcagg | cttctgggga | aagaaagcca | gctgaatttt | gactccatct | 1740 |
| ccccagaaga | tgctgggagt | tacagctgct | gggtgaacaa | ctccatagga | cagacagcgt | 1800 |
| ccaaggcctg | gacacttgaa | gtgctgtatg | cacccaggag | gctgctgtg | tccatgagcc | 1860 |
| cgggggacca | agtgatggag | gggaagagtg | caaccctgac | ctgtgagagt | gacgccaacc | 1920 |
| ctcccgtctc | ccactacacc | tggtttgact | ggaataacca | aagcctcccc | caccacagcc | 1980 |
| agaagctgag | attggagccg | gtgaagggtcc | agcactcggg | tgctactggg | tgccagggga | 2040 |
| ccaacagtgt | gggcaagggc | cgttcgcttc | tcagcaccct | tactgtctac | tatagcccgg | 2100 |
| agaccatcgg | caggcgagtg | gctgtgggac | tcgggtcctg | cctcgccatc | ctcatcctgg | 2160 |
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| aggagaattc | cagcggccag | agcttctttg | tgaggaataa | aaaggttaga | agggccccc | 2280 |
| tctctgaagg | ccccactcc | ctgggatgct | acaatccaat | gatggaagat | ggcattagct | 2340 |
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| acctcccctg | ccccaccagc | ccactggcca | tctccaccg | gagctgctgt | gtcctctgga | 2940 |
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<400> 133

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| | | | 20 | | | | 25 | | | | | 30 | | | |
| Tyr | Ala | Trp | Glu | Gly | Ala | Cys | Val | Trp | Ile | Pro | Cys | Thr | Tyr | Arg | Ala |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Leu | Asp | Gly | Asp | Leu | Glu | Ser | Phe | Ile | Leu | Phe | His | Asn | Pro | Glu | Tyr |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Asn | Lys | Asn | Thr | Ser | Lys | Phe | Asp | Gly | Thr | Arg | Leu | Tyr | Glu | Ser | Thr |
| | 65 | | | | 70 | | | | | 75 | | | | | 80 |
| Lys | Asp | Gly | Lys | Val | Pro | Ser | Glu | Gln | Lys | Arg | Val | Gln | Phe | Leu | Gly |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Asp | Lys | Asn | Lys | Asn | Cys | Thr | Leu | Ser | Ile | His | Pro | Val | His | Leu | Asn |
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| Asp | Ser | Gly | Gln | Leu | Gly | Leu | Arg | Met | Glu | Ser | Lys | Thr | Glu | Lys | Trp |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Met | Glu | Arg | Ile | His | Leu | Asn | Val | Ser | Glu | Arg | Pro | Phe | Pro | Pro | His |
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| Ile | Gln | Leu | Pro | Pro | Glu | Ile | Gln | Glu | Ser | Gln | Glu | Val | Thr | Leu | Thr |
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| Cys | Leu | Leu | Asn | Phe | Ser | Cys | Tyr | Gly | Tyr | Pro | Ile | Gln | Leu | Gln | Trp |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| Leu | Leu | Glu | Gly | Val | Pro | Met | Arg | Gln | Ala | Ala | Val | Thr | Ser | Thr | Ser |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Leu | Thr | Ile | Lys | Ser | Val | Phe | Thr | Arg | Ser | Glu | Leu | Lys | Phe | Ser | Pro |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Gln | Trp | Ser | His | His | Gly | Lys | Ile | Val | Thr | Cys | Gln | Leu | Gln | Asp | Ala |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Asp | Gly | Lys | Phe | Leu | Ser | Asn | Asp | Thr | Val | Gln | Leu | Asn | Val | Lys | His |
| | 225 | | | | 230 | | | | | 235 | | | | | 240 |
| Thr | Pro | Lys | Leu | Glu | Ile | Lys | Val | Thr | Pro | Ser | Asp | Ala | Ile | Val | Arg |
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WO 2005/037989

PCT/US2003/024918

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 Gly Lys Tyr Cys Cys Gln Val Ser Asn Asp Val Gly Pro Gly Arg Ser
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 Glu Glu Val Phe Leu Gln Val Gln Tyr Ala Pro Glu Pro Ser Thr Val
 325 330 335
 Gln Ile Leu His Ser Pro Ala Val Glu Gly Ser Gln Val Glu Phe Leu
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 Cys Met Ser Leu Ala Asn Pro Leu Pro Thr Asn Tyr Thr Trp Tyr His
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 Asn Gly Lys Glu Met Gln Gly Arg Thr Glu Glu Lys Val His Ile Pro
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 Tyr Pro Pro Lys Lys Val Thr Thr Val Ile Gln Asn Pro Met Pro Ile
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 Gly Lys Ser Ala Thr Leu Thr Cys Glu Ser Asp Ala Asn Pro Pro Val
 610 615 620
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 625 630 635 640
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 675 680 685
 Ala Val Gly Leu Gly Ser Cys Leu Ala Ile Leu Ile Leu Ala Ile Cys
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 Gly Leu Lys Leu Gln Arg Arg Trp Lys Arg Thr Gln Ser Gln Gln Gly
 705 710 715 720
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 725 730 735
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 755 760 765
 Glu Met Asn Ile Pro Arg Thr Gly Asp Ala Glu Ser Ser Glu Met Gln
 770 775 780
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WO 2005/037989

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 <213> Homo sapiens

<400> 135
 Met Asp Pro Gly Leu Gln Gln Ala Leu Asn Gly Met Ala Pro Pro Gly
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 Asp Thr Ala Met His Val Pro Ala Gly Ser Val Ala Ser His Leu Gly
 20 25 30
 Thr Thr Ser Arg Ser Tyr Phe Tyr Leu Thr Thr Ala Thr Leu Ala Leu
 35 40 45
 Cys Leu Val Phe Thr Val Ala Thr Ile Met Val Leu Val Val Gln Arg
 50 55 60
 Thr Asp Ser Ile Pro Asn Ser Pro Asp Asn Val Pro Leu Lys Gly Gly
 65 70 75 80
 Asn Cys Ser Glu Asp Leu Leu Cys Ile Leu Lys Arg Ala Pro Phe Lys
 85 90 95
 Lys Ser Trp Ala Tyr Leu Gln Val Ala Lys His Leu Asn Lys Thr Lys
 100 105 110
 Leu Ser Trp Asn Lys Asp Gly Ile Leu His Gly Val Arg Tyr Gln Asp
 115 120 125
 Gly Asn Leu Val Ile Gln Phe Pro Gly Leu Tyr Phe Ile Ile Cys Gln

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

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|---|-----|-----|
| 130 | 135 | 140 |
| Leu Gln Phe Leu Val Gln Cys Pro Asn Asn Ser Val Asp Leu Lys Leu | | |
| 145 | 150 | 155 |
| Glu Leu Leu Ile Asn Lys His Ile Lys Lys Gln Ala Leu Val Thr Val | | |
| | 165 | 170 |
| Cys Glu Ser Gly Met Gln Thr Lys His Val Tyr Gln Asn Leu Ser Gln | | |
| | 180 | 185 |
| Phe Leu Leu Asp Tyr Leu Gln Val Asn Thr Thr Ile Ser Val Asn Val | | |
| | 195 | 200 |
| Asp Thr Phe Gln Tyr Ile Asp Thr Ser Thr Phe Pro Leu Glu Asn Val | | |
| | 210 | 215 |
| Leu Ser Ile Phe Leu Tyr Ser Asn Ser Asp | | |
| 225 | 230 | |

<210> 136
<211> 1125
<212> DNA
<213> Homo sapiens

<400> 136

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| aagatgtcag | cccaggagag | ctgcctcagc | ctcatcaagt | acttcctctt | cgttttcaac | 120 |
| ctcttcttct | tcgtcctcgg | cagcctgata | ttctgcttcg | gcattctggat | cctcatcgac | 180 |
| aagaccagct | tcgtgtcctt | tgtgggcttg | gccttcgtgc | ctctgcagat | ctgggtccaaa | 240 |
| gtcctggcca | tctcaggaat | cttcaccatg | ggcatcgccc | tcctgggttg | tgtgggggcc | 300 |
| ctcaaggagc | tccgtgcctt | cctgggcctg | tattttggga | tgctgctgct | cctgtttgcc | 360 |
| acacagatca | ccctgggaat | cctcatctcc | actcagcggg | cccagctgga | gcgaagcttg | 420 |
| cgggacgtcg | tagagaaaac | catccaaaag | tacggcacca | accccgagga | gaccgcggcc | 480 |
| gaggagagct | gggactatgt | gcagttccag | ctgcgctgct | gcggctggca | ctaccgcag | 540 |
| gactggttcc | aagtcctcat | cctgagaggt | aacgggtcgg | aggcgaccg | cgctccctgc | 600 |
| tcctgctaca | acttgctggc | gaccaacgac | tccacaatcc | tagataaggt | gatcttgccc | 660 |
| cagctcagca | ggcttggaca | cctggcgcgg | tccagacaca | gtgcagacat | ctgcgctgct | 720 |
| cctgcagaga | gccacatcta | ccgcgagggc | tgcgcgagg | gcctccagaa | gtggctgcac | 780 |
| aacaacctta | tttccatagt | gggcatttgc | ctgggcgtcg | gcctactcga | gctcgggttc | 840 |
| atgacgctct | cgatattcct | gtgcagaaac | ctggaccacg | tctacaaccg | gctcgtctga | 900 |
| taccgttagg | ccccgccctc | cccaaagtc | cgccccgcc | ccgtcacgtg | cgctggggac | 960 |
| ttccctgctg | cctgtaaata | tttgtttaat | cccaggttcg | cctggagccc | tccgcttca | 1020 |
| cattcccttg | gggacccacg | tggtgcgtg | ccctgctgc | tgtcacctct | cccacgggac | 1080 |
| ctggggcctt | cgtccacagc | ttcctgtccc | catctgtcgg | cctac | | 1125 |

<210> 137
<211> 281
<212> PRT
<213> Homo sapiens

<400> 137

| | |
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| Val Phe Asn Leu Phe Phe Phe Val Leu Gly Ser Leu Ile Phe Cys Phe | |
| 20 25 30 | |
| Gly Ile Trp Ile Leu Ile Asp Lys Thr Ser Phe Val Ser Phe Val Gly | |
| 35 40 45 | |
| Leu Ala Phe Val Pro Leu Gln Ile Trp Ser Lys Val Leu Ala Ile Ser | |
| 50 55 60 | |
| Gly Ile Phe Thr Met Gly Ile Ala Leu Leu Gly Cys Val Gly Ala Leu | |
| 65 70 75 80 | |
| Lys Glu Leu Arg Cys Leu Leu Gly Leu Tyr Phe Gly Met Leu Leu Leu | |
| 85 90 95 | |
| Leu Phe Ala Thr Gln Ile Thr Leu Gly Ile Leu Ile Ser Thr Gln Arg | |
| 100 105 110 | |
| Ala Gln Leu Glu Arg Ser Leu Arg Asp Val Val Glu Lys Thr Ile Gln | |
| 115 120 125 | |
| Lys Tyr Gly Thr Asn Pro Glu Glu Thr Ala Ala Glu Glu Ser Trp Asp | |
| 130 135 140 | |
| Tyr Val Gln Phe Gln Leu Arg Cys Cys Gly Trp His Tyr Pro Gln Asp | |
| 145 150 155 160 | |
| Trp Phe Gln Val Leu Ile Leu Arg Gly Asn Gly Ser Glu Ala His Arg | |
| 165 170 175 | |

WO 2005/037989

PCT/US2003/024918

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Val Pro Cys Ser Cys Tyr Asn Leu Ser Ala Thr Asn Asp Ser Thr Ile
180 185 190
Leu Asp Lys Val Ile Leu Pro Gln Leu Ser Arg Leu Gly His Leu Ala
195 200 205
Arg Ser Arg His Ser Ala Asp Ile Cys Ala Val Pro Ala Glu Ser His
210 215 220
Ile Tyr Arg Glu Gly Cys Ala Gln Gly Leu Gln Lys Trp Leu His Asn
225 230 235 240
Asn Leu Ile Ser Ile Val Gly Ile Cys Leu Gly Val Gly Leu Leu Glu
245 250 255
Leu Gly Phe Met Thr Leu Ser Ile Phe Leu Cys Arg Asn Leu Asp His
260 265 270
Val Tyr Asn Arg Leu Ala Arg Tyr Arg
275 280

<210> 138
<211> 2220
<212> DNA
<213> Homo sapiens

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gactccgtct cattgacttg cagcaccaca ggctgtgagt ccccatTTTT ctcttggaga 180
accagatag atagtccact gaatgggaag gtgacgaatg aggggaccac atctacgctg 240
acaatgaatc ctgttagttt tgggaacgaa cactcttacc tgtgcacagc aacttgtgaa 300
tctaggaaat tggaaaaagg aatccaggtg gagatctact ctttctctaa ggatccagag 360
attcatttga gtggccctct ggaggctggg aagccgatca cagtcaagtg ttcagttgct 420
gatgtatacc catttgacag gctggagata gacttactga aaggagatca tctcatgaag 480
agtcaggaat ttctggagga tgcagacagg aagtccctgg aaaccaagag tttggaagta 540
acctttactc ctgtcattga ggatatttga aaagtctctg tttgccgagc taaattacac 600
attgatgaaa tggattctgt gccacagta aggcaggctg taaaagaatt gcaagtctac 660
atatcaccca agaatacagt tatttctgtg aatccatcca caaagctgca agaaggtggc 720
tctgtgacca tgacctgttc cagcgagggt ctaccagctc cagagatttt ctggagtaag 780
aaatcccatc atgggaatct acagcacctt tctggaaatg caactctcac ctttaattgct 840
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ccccgattg ctgtcagat tggagactca gtcatgttga catgtagtgt catgggctgt 1020
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agtgagggga ccaattccac gctgaccctg agccctgtga gttttgagaa cgaacactct 1140
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tactcatccc ctagagatcc agaaatcgag atgagtgggt gcctcgtgaa tgggagctct 1260
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cttaaggggg agactattct ggagaatata gagtttttgg aggatacggg tatgaaatct 1380
ctagagaaca aaagtttggg aatgaccttc atccctacca ttgaagatac tggaaaagct 1440
cttgtttgtc aggctaagtt acatattgat gacatggaat tcgaacccaa acaaaaggcag 1500
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tcctccatcc tggaggaagg cagttctgtg aatatgacat gcttgagcca gggctttcct 1620
gctccgaaaa tcctgtggag caggcagctc cctaaccggg agctacagcc tctttctgag 1680
aatgcaactc tcaccttaat ttctacaaaa atggaagatt ctgggggttta tttatgtgaa 1740
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acaggagaca cagtactaaa atctatagat ggcgcctata ccatccgaaa ggcccagttg 1980
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gtgctctatt ttgcatcctc cttaataata cctgccattg gaatgataat ttacttttga 2160
agaaaagcca acatgaaggg gtcatatagt cttgtagaag cacagaaatc aaaagtgtag 2220

<210> 139
<211> 739
<212> PRT
<213> Homo sapiens

<400> 139
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1 5 10 15

WO 2005/037989

PCT/US2003/024918

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 Ser Arg Tyr Leu Ala Gln Ile Gly Asp Ser Val Ser Leu Thr Cys Ser
 35 40 45
 Thr Thr Gly Cys Glu Ser Pro Phe Phe Ser Trp Arg Thr Gln Ile Asp
 50 55 60
 Ser Pro Leu Asn Gly Lys Val Thr Asn Glu Gly Thr Thr Ser Thr Leu
 65 70 75 80
 Thr Met Asn Pro Val Ser Phe Gly Asn Glu His Ser Tyr Leu Cys Thr
 85 90 95
 Ala Thr Cys Glu Ser Arg Lys Leu Glu Lys Gly Ile Gln Val Glu Ile
 100 105 110
 Tyr Ser Phe Pro Lys Asp Pro Glu Ile His Leu Ser Gly Pro Leu Glu
 115 120 125
 Ala Gly Lys Pro Ile Thr Val Lys Cys Ser Val Ala Asp Val Tyr Pro
 130 135 140
 Phe Asp Arg Leu Glu Ile Asp Leu Leu Lys Gly Asp His Leu Met Lys
 145 150 155 160
 Ser Gln Glu Phe Leu Glu Asp Ala Asp Arg Lys Ser Leu Glu Thr Lys
 165 170 175
 Ser Leu Glu Val Thr Phe Thr Pro Val Ile Glu Asp Ile Gly Lys Val
 180 185 190
 Leu Val Cys Arg Ala Lys Leu His Ile Asp Glu Met Asp Ser Val Pro
 195 200 205
 Thr Val Arg Gln Ala Val Lys Glu Leu Gln Val Tyr Ile Ser Pro Lys
 210 215 220
 Asn Thr Val Ile Ser Val Asn Pro Ser Thr Lys Leu Gln Glu Gly Gly
 225 230 235 240
 Ser Val Thr Met Thr Cys Ser Ser Glu Gly Leu Pro Ala Pro Glu Ile
 245 250 255
 Phe Trp Ser Lys Lys Leu Asp Asn Gly Asn Leu Gln His Leu Ser Gly
 260 265 270
 Asn Ala Thr Leu Thr Leu Ile Ala Met Arg Met Glu Asp Ser Gly Ile
 275 280 285
 Tyr Val Cys Glu Gly Val Asn Leu Ile Gly Lys Asn Arg Lys Glu Val
 290 295 300
 Glu Leu Ile Val Gln Glu Lys Pro Phe Thr Val Glu Ile Ser Pro Gly
 305 310 315 320
 Pro Arg Ile Ala Ala Gln Ile Gly Asp Ser Val Met Leu Thr Cys Ser
 325 330 335
 Val Met Gly Cys Glu Ser Pro Ser Phe Ser Trp Arg Thr Gln Ile Asp
 340 345 350
 Ser Pro Leu Ser Gly Lys Val Arg Ser Glu Gly Thr Asn Ser Thr Leu
 355 360 365
 Thr Leu Ser Pro Val Ser Phe Glu Asn Glu His Ser Tyr Leu Cys Thr
 370 375 380
 Val Thr Cys Gly His Lys Lys Leu Glu Lys Gly Ile Gln Val Glu Leu
 385 390 395 400
 Tyr Ser Phe Pro Arg Asp Pro Glu Ile Glu Met Ser Gly Gly Leu Val
 405 410 415
 Asn Gly Ser Ser Val Thr Val Ser Cys Lys Val Pro Ser Val Tyr Pro
 420 425 430
 Leu Asp Arg Leu Glu Ile Glu Leu Leu Lys Gly Glu Thr Ile Leu Glu
 435 440 445
 Asn Ile Glu Phe Leu Glu Asp Thr Asp Met Lys Ser Leu Glu Asn Lys
 450 455 460
 Ser Leu Glu Met Thr Phe Ile Pro Thr Ile Glu Asp Thr Gly Lys Ala
 465 470 475 480
 Leu Val Cys Gln Ala Lys Leu His Ile Asp Asp Met Glu Phe Glu Pro
 485 490 495
 Lys Gln Arg Gln Ser Thr Gln Thr Leu Tyr Val Asn Val Ala Pro Arg
 500 505 510
 Asp Thr Thr Val Leu Val Ser Pro Ser Ser Ile Leu Glu Gly Ser
 515 520 525
 Ser Val Asn Met Thr Cys Leu Ser Gln Gly Phe Pro Ala Pro Lys Ile
 530 535 540
 Leu Trp Ser Arg Gln Leu Pro Asn Gly Glu Leu Gln Pro Leu Ser Glu
 545 550 555 560
 Asn Ala Thr Leu Thr Leu Ile Ser Thr Lys Met Glu Asp Ser Gly Val

WO 2005/037989

PCT/US2003/024918

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 565 570 575
 Tyr Leu Cys Glu Gly Ile Asn Gln Ala Gly Arg Ser Arg Lys Glu Val
 580 585 590
 Glu Leu Ile Ile Gln Val Thr Pro Lys Asp Ile Lys Leu Thr Ala Phe
 595 600 605
 Pro Ser Glu Ser Val Lys Glu Gly Asp Thr Val Ile Ile Ser Cys Thr
 610 615 620
 Cys Gly Asn Val Pro Glu Thr Trp Ile Ile Leu Lys Lys Lys Ala Glu
 625 630 635 640
 Thr Gly Asp Thr Val Leu Lys Ser Ile Asp Gly Ala Tyr Thr Ile Arg
 645 650 655
 Lys Ala Gln Leu Lys Asp Ala Gly Val Tyr Glu Cys Glu Ser Lys Asn
 660 665 670
 Lys Val Gly Ser Gln Leu Arg Ser Leu Thr Leu Asp Val Gln Gly Arg
 675 680 685
 Glu Asn Asn Lys Asp Tyr Phe Ser Pro Glu Leu Leu Val Leu Tyr Phe
 690 695 700
 Ala Ser Ser Leu Ile Ile Pro Ala Ile Gly Met Ile Ile Tyr Phe Ala
 705 710 715 720
 Arg Lys Ala Asn Met Lys Gly Ser Tyr Ser Leu Val Glu Ala Gln Lys
 725 730 735
 Ser Lys Val

<210> 140
 <211> 2986
 <212> DNA
 <213> Homo sapiens

<400> 140
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 ccaggacctg gcaatgcccc gacatctgtg tccccctcaa aagtcacctc gccccgggga 180
 ggctccgtgc tggtagcatg cagcacctcc tgtgaccagc ccaagttggt gggcatagag 240
 accccgttgc ctaaaaagga gttgctcctg cctgggaaca accggaaggt gtatgaactg 300
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 ccccgggcca acctcacctg ggtgctgctc cgtggggaga aggagctgaa acgggagcca 540
 gctgtggggg agcccgctga ggtcacgacc acgggtgctg tgaggagaga tcaccatgga 600
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 aacacctcgg ccccttaccg gctccagacc tttgtcctgc cagcgactcc ccacaaactt 720
 ggggtcctaga ggtggacacg caggggacct tgggtctgtt cctgacaggg 780
 ctgttcccg tctcgagggc ccagggtccac ctggcactgg gggaccagag gttgaacccc 840
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 atacacaaga accagacctg ggagcttctg gtcctgtatg gccccgact ggacgagag 1260
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WO 2005/037989

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 atggactggg aatggttcac aggttcagag attaccaggt gaggccttat tcctcccttc 2460
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 ttggggctca agtgatctc ccacctcagc ctctgagta gctgggacca taggctcaca 2880
 acaccacacc tggcaaatat gatttttttt ttttttttca gagacggggg ctgcaacat 2940
 tgcccagact tcctttgtgt tagttaataa agctttctca actgcc 2986

<210> 141
 <211> 532
 <212> PRT
 <213> Homo sapiens

<400> 141
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 Leu Gly Ala Leu Phe Pro Gly Pro Gly Asn Ala Gln Thr Ser Val Ser
 20 25 30
 Pro Ser Lys Val Ile Leu Pro Arg Gly Gly Ser Val Leu Val Thr Cys
 35 40 45
 Ser Thr Ser Cys Asp Gln Pro Lys Leu Leu Gly Ile Glu Thr Pro Leu
 50 55 60
 Pro Lys Lys Glu Leu Leu Leu Pro Gly Asn Asn Arg Lys Val Tyr Glu
 65 70 75 80
 Leu Ser Asn Val Gln Glu Asp Ser Gln Pro Met Cys Tyr Ser Asn Cys
 85 90 95
 Pro Asp Gly Gln Ser Thr Ala Lys Thr Phe Leu Thr Val Tyr Trp Thr
 100 105 110
 Pro Glu Arg Val Glu Leu Ala Pro Leu Pro Ser Trp Gln Pro Val Gly
 115 120 125
 Lys Asn Leu Thr Leu Arg Cys Gln Val Glu Gly Gly Ala Pro Arg Ala
 130 135 140
 Asn Leu Thr Val Val Leu Leu Arg Gly Glu Lys Glu Leu Lys Arg Glu
 145 150 155 160
 Pro Ala Val Gly Glu Pro Ala Glu Val Thr Thr Thr Val Leu Val Arg
 165 170 175
 Arg Asp His His Gly Ala Asn Phe Ser Cys Arg Thr Glu Leu Asp Leu
 180 185 190
 Arg Pro Gln Gly Leu Glu Leu Phe Glu Asn Thr Ser Ala Pro Tyr Gln
 195 200 205
 Leu Gln Thr Phe Val Leu Pro Ala Thr Pro Pro Gln Leu Val Ser Pro
 210 215 220
 Arg Val Leu Glu Val Asp Thr Gln Gly Thr Val Val Cys Ser Leu Asp
 225 230 235 240
 Gly Leu Phe Pro Val Ser Glu Ala Gln Val His Leu Ala Leu Gly Asp
 245 250 255
 Gln Arg Leu Asn Pro Thr Val Thr Tyr Gly Asn Asp Ser Phe Ser Ala
 260 265 270
 Lys Ala Ser Val Ser Val Thr Ala Glu Asp Glu Gly Thr Gln Arg Leu
 275 280 285
 Thr Cys Ala Val Ile Leu Gly Asn Gln Ser Gln Glu Thr Leu Gln Thr
 290 295 300
 Val Thr Ile Tyr Ser Phe Pro Ala Pro Asn Val Ile Leu Thr Lys Pro
 305 310 315 320
 Glu Val Ser Glu Gly Thr Glu Val Thr Val Lys Cys Glu Ala His Pro
 325 330 335
 Arg Ala Lys Val Thr Leu Asn Gly Val Pro Ala Gln Pro Leu Gly Pro
 340 345 350
 Arg Ala Gln Leu Leu Lys Ala Thr Pro Glu Asp Asn Gly Arg Ser
 355 360 365
 Phe Ser Cys Ser Ala Thr Leu Glu Val Ala Gly Gln Leu Ile His Lys
 370 375 380
 Asn Gln Thr Arg Glu Leu Arg Val Leu Tyr Gly Pro Arg Leu Asp Glu
 385 390 395 400

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 Arg Asp Cys Pro Gly Asn Trp Thr Trp Pro Glu Asn Ser Gln Gln Thr
 405 410 415
 Pro Met Cys Gln Ala Trp Gly Asn Pro Leu Pro Glu Leu Lys Cys Leu
 420 425 430
 Lys Asp Gly Thr Phe Pro Leu Pro Ile Gly Glu Ser Val Thr Val Thr
 435 440 445
 Arg Asp Leu Glu Gly Thr Tyr Leu Cys Arg Ala Arg Ser Thr Gln Gly
 450 455 460
 Glu Val Thr Arg Glu Val Thr Val Asn Val Leu Ser Pro Arg Tyr Glu
 465 470 475 480
 Ile Val Ile Ile Thr Val Val Ala Ala Val Ile Met Gly Thr Ala
 485 490 495
 Gly Leu Ser Thr Tyr Leu Tyr Asn Arg Gln Arg Lys Ile Lys Lys Tyr
 500 505 510
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 Ala Thr Pro Pro
 530

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 <212> DNA
 <213> Mus musculus

<400> 142
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 tgggacccgc agctctccta tgcagtgtcc tgggccaagg tctccgagag tggcactgag 180
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 caggagctcg gagggcagcg caacttgagc ggcaaccgtg ttctgaaggc gacaggatgc 360
 cccaaggaag ctacagagtc aactttcagg aagtacaggg cagaagctgt gttgctcttc 420
 tctctggttg ttttctacct gacactcatc attttcacct gcaaatttgc acgactacaa 480
 agcattttcc cagatatttc taaacctggc acggaacaag cttttcttcc agtcacctcc 540
 ccaagcaaac atttggggcc agtgaccctt cctaagacag aaacgggatg a 591

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 <211> 196
 <212> PRT
 <213> Mus musculus

<400> 143
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 20 25 30
 Ala Asp Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln Leu Ser Tyr Ala
 35 40 45
 Val Ser Trp Ala Lys Val Ser Glu Ser Gly Thr Glu Ser Val Glu Leu
 50 55 60
 Pro Glu Ser Lys Gln Asn Ser Ser Phe Glu Ala Pro Arg Arg Arg Ala
 65 70 75 80
 Tyr Ser Leu Thr Ile Gln Asn Thr Thr Ile Cys Ser Ser Gly Thr Tyr
 85 90 95
 Arg Cys Ala Leu Gln Glu Leu Gly Gly Gln Arg Asn Leu Ser Gly Thr
 100 105 110
 Val Val Leu Lys Val Thr Gly Cys Pro Lys Glu Ala Thr Glu Ser Thr
 115 120 125
 Phe Arg Lys Tyr Arg Ala Glu Ala Val Leu Leu Phe Ser Leu Val Val
 130 135 140
 Phe Tyr Leu Thr Leu Ile Phe Thr Cys Lys Phe Ala Arg Leu Gln
 145 150 155 160
 Ser Ile Phe Pro Asp Ile Ser Lys Pro Gly Thr Glu Gln Ala Phe Leu
 165 170 175
 Pro Val Thr Ser Pro Ser Lys His Leu Gly Pro Val Thr Leu Pro Lys
 180 185 190
 Thr Glu Thr Val
 195